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(54) Title: COMPOSITIONS AND METHODS FOR THE TREATMENT OF IMMUNE RELATED DISEASES

(57) Abstract: The present invention relates to compositions containing novel proteins and methods of using those compositions for the diagnosis and treatment of immune related diseases.

**COMPOSITIONS AND METHODS FOR THE TREATMENT OF IMMUNE RELATED DISEASES****PRIORITY**

5 This application claims priority to U.S. Provisional Application No.: 60/493,546 filed August 11, 2003, to which U.S. Provisional Applications claim priority under 35 U.S.C. §119, the entire disclosure of which is hereby incorporated by reference in its entirety.

**FIELD OF THE INVENTION**

10 The present invention relates to compositions and methods useful for the diagnosis and treatment of immune related diseases.

**BACKGROUND OF THE INVENTION**

15 Immune related and inflammatory diseases are the manifestation or consequence of fairly complex, often multiple interconnected biological pathways which in normal physiology are critical to respond to insult or injury, initiate repair from insult or injury, and mount innate and acquired defense against foreign organisms. Disease or pathology occurs when these normal physiological pathways cause additional insult or injury either as directly related to the intensity of the response, as a consequence of abnormal regulation or excessive stimulation, as a reaction to self, or as a combination of these.

20 Though the genesis of these diseases often involves multistep pathways and often multiple different biological systems/pathways, intervention at critical points in one or more of these pathways can have an ameliorative or therapeutic effect. Therapeutic intervention can occur by either antagonism of a detrimental process/pathway or stimulation of a beneficial process/pathway.

25 Many immune related diseases are known and have been extensively studied. Such diseases include immune-mediated inflammatory diseases, non-immune-mediated inflammatory diseases, infectious diseases, immunodeficiency diseases, neoplasia, etc.

30 T lymphocytes (T cells) are an important component of a mammalian immune response. T cells recognize antigens which are associated with a self-molecule encoded by genes within the major histocompatibility complex (MHC). The antigen may be displayed together with MHC molecules on the surface of antigen presenting cells, virus infected cells, cancer cells, grafts, etc. The T cell system eliminates these altered cells which pose a health threat to the host mammal. T cells include helper T cells and cytotoxic T cells. Helper T cells proliferate extensively following recognition of an antigen -MHC complex on an antigen presenting cell. Helper T cells also secrete a variety of cytokines, i.e., lymphokines, which play a central role in the activation of B cells, cytotoxic T cells and a variety of other cells which participate 35 in the immune response.

CD4 T helper cells play central role in regulating immune system. Under different pathogenic challenges, naive CD4 T cells can differentiate to two different subsets. T helper 1 (Th1) cells produce IFN-gamma, TNF-alpha and LT. Th1 cells and cytokines they produced are important for cellular immunity and critical for clearance of intracellular pathogen invasions. IFN-gamma produced by Th1 cells also helps 40 antibody isotype switch to IgG2a, while the cytokines produced by Th1 cells activate macrophages and

promote CTL reaction. In contrast, T helper 2 (Th2) CD4 cells mainly mediate humoral immunity. Th2 cells secrete IL-4, IL-5, IL-6, and IL-13. These cytokines play central role in promotion of eosinophil development and mast cell activation. Th2 cells also help in B cell development antibody isotype switching to IgE and IgA. Th2 cells and their cytokines are critical for helminthes clearance.

5        Although Th1 and Th2 cells are necessary for the immune system to fight with various pathogenic invasion, unregulated Th1 and Th2 differentiation could play a role in autoimmune diseases. For example, uncontrolled Th2 differentiation has been demonstrated to be involved in immediate hypersensitivity, allergic reaction and asthma. Th1 cells have been shown to present in diabetes, MS, psoriasis, and lupus. Currently, IL-12 and IL-4 have been identified to be the key cytokines initiating the development of the Th1  
10      and Th2 cells, respectively. Upon binding to its receptor, IL-12 activates Stat4, which then forms a homodimer, migrates into the nucleus and initiates down stream transcription events for Th1 development. IL-4 activates a different Stat molecule, Stat6, which induces transcription factor GATA3 expression. GATA-3 will then promote downstream differentiation of Th2 cells. The differentiation of Th1 and Th2 cells are a dynamic process, at each stage, there are different molecular events happening and different gene  
15      expression profiles. For example, at the early stage naive T cells are sensitive to environment stimuli, such as cytokines and costimulatory signals. If they receive the Th2 priming signal, they will quickly shut down the expression of the IL-12 receptor b2 chain expression and block further Th1 development. However, at the late stage of Th1 development, applying Th2 differentiation cytokines will fail to switch cells to a Th2 type. In this experiment, we mapped the gene expression profiles during the whole process of Th1 and Th2  
20      development. We isolated naive CD4 T cells from normal human donors. Th1 cells were generated by stimulation of T cells with anti-CD3 and CD-28 plus IL-12, and anti-IL-4 antibody. Th2 cells were generated by similar TCR stimulation plus IL-4, anti-IL12, and anti-IFN-g antibodies. The undifferentiated T cells were generated by TCR stimulation, and neutralizing antibodies for IL-12, IL-4 and IFN-gamma. T cells were expanded on day 3 of primary activation with 5 volumes of fresh media. The fully differentiated  
25      Th1 and Th2 cells were then restimulated by anti-CD3 and anti-CD28. RNA was purified at different stages of T cell development, and RNA isolated for gene chip based expression analysis. Comparing gene expression profiles enabled us to identified genes preferentially expressed in Th1 or Th2 cell at different stages. These genes could play very important roles in the initiation of Th1/Th2 differentiation, maintenance of Th1/Th2 phenotype, activation of Th1/Th2 cells, and effector functions, such as cytokine production, of  
30      Th1/Th2 cells. These genes could also serve as molecular markers to identify and target specific Th1 and Th2 subsets. Thus, these genes are potential therapeutic targets for many autoimmune diseases.

Autoimmune related diseases could be treated by suppressing the immune response. Using neutralizing antibodies that inhibit molecules having immune stimulatory activity would be beneficial in the treatment of immune-mediated and inflammatory diseases. Molecules which inhibit the immune response  
35      can be utilized (proteins directly or via the use of antibody agonists) to inhibit the immune response and thus ameliorate immune related disease.

Despite the above identified advances in T cell research, there is a great need for additional diagnostic and therapeutic agents capable of detecting the presence of a T cell mediated disorders in a mammal and for effectively reducing these disorders. Accordingly, it is an objective of the present invention  
40      to identify polypeptides that are overexpressed in activated T cells as compared to resting T cells, and to use

those polypeptides, and their encoding nucleic acids, to produce compositions of matter useful in the therapeutic treatment and diagnostic detection of T cell mediated disorders in mammals.

SUMMARY OF THE INVENTIONA. Embodiments

The present invention concerns compositions and methods useful for the diagnosis and treatment of immune related disease in mammals, including humans. The present invention is based on the identification 5 of proteins (including agonist and antagonist antibodies) which are a result of stimulation of the immune response in mammals. Immune related diseases can be treated by suppressing or enhancing the immune response. Molecules that enhance the immune response stimulate or potentiate the immune response to an antigen. Molecules which stimulate the immune response can be used therapeutically where enhancement of the immune response would be beneficial. Alternatively, molecules that suppress the immune response 10 attenuate or reduce the immune response to an antigen (e.g., neutralizing antibodies) can be used therapeutically where attenuation of the immune response would be beneficial (e.g., inflammation). Accordingly, the PRO polypeptides, agonists and antagonists thereof are also useful to prepare medicines and medicaments for the treatment of immune-related and inflammatory diseases. In a specific aspect, such medicines and medicaments comprise a therapeutically effective amount of a PRO polypeptide, agonist or 15 antagonist thereof with a pharmaceutically acceptable carrier. Preferably, the admixture is sterile.

In a further embodiment, the invention concerns a method of identifying agonists or antagonists to a PRO polypeptide which comprises contacting the PRO polypeptide with a candidate molecule and monitoring a biological activity mediated by said PRO polypeptide. Preferably, the PRO polypeptide is a native sequence PRO polypeptide. In a specific aspect, the PRO agonist or antagonist is an anti-PRO 20 antibody.

In another embodiment, the invention concerns a composition of matter comprising a PRO polypeptide or an agonist or antagonist antibody which binds the polypeptide in admixture with a carrier or excipient. In one aspect, the composition comprises a therapeutically effective amount of the polypeptide or antibody. In another aspect, when the composition comprises an immune stimulating molecule, the 25 composition is useful for: (a) increasing infiltration of inflammatory cells into a tissue of a mammal in need thereof, (b) stimulating or enhancing an immune response in a mammal in need thereof, (c) increasing the proliferation of T-lymphocytes in a mammal in need thereof in response to an antigen, (d) stimulating the activity of T-lymphocytes or (e) increasing the vascular permeability. In a further aspect, when the composition comprises an immune inhibiting molecule, the composition is useful for: (a) decreasing infiltration of inflammatory cells into a tissue of a mammal in need thereof, (b) inhibiting or reducing an 30 immune response in a mammal in need thereof, (c) decreasing the activity of T-lymphocytes or (d) decreasing the proliferation of T-lymphocytes in a mammal in need thereof in response to an antigen. In another aspect, the composition comprises a further active ingredient, which may, for example, be a further antibody or a cytotoxic or chemotherapeutic agent. Preferably, the composition is sterile.

35 In another embodiment, the invention concerns a method of treating an immune related disorder in a mammal in need thereof, comprising administering to the mammal an effective amount of a PRO polypeptide, an agonist thereof, or an antagonist thereto. In a preferred aspect, the immune related disorder is selected from the group consisting of: systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis, spondyloarthropathies, systemic sclerosis, idiopathic inflammatory myopathies, 40 Sjögren's syndrome, systemic vasculitis, sarcoidosis, autoimmune hemolytic anemia, autoimmune

thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal disease, demyelinating diseases of the central and peripheral nervous systems such as multiple sclerosis, idiopathic demyelinating polyneuropathy or Guillain-Barré syndrome, and chronic inflammatory demyelinating polyneuropathy, hepatobiliary diseases such as infectious, autoimmune chronic active hepatitis, primary biliary cirrhosis, 5 granulomatous hepatitis, and sclerosing cholangitis; inflammatory bowel disease, gluten-sensitive enteropathy, and Whipple's disease, autoimmune or immune-mediated skin diseases including bullous skin diseases, erythema multiforme and contact dermatitis, psoriasis, allergic diseases such as asthma, allergic rhinitis, atopic dermatitis, food hypersensitivity and urticaria, immunologic diseases of the lung such as eosinophilic pneumonias, idiopathic pulmonary fibrosis and hypersensitivity pneumonitis, transplantation 10 associated diseases including graft rejection and graft -versus-host-disease.

In another embodiment, the invention provides an antibody which specifically binds to any of the above or below described polypeptides. Optionally, the antibody is a monoclonal antibody, humanized antibody, antibody fragment or single-chain antibody. In one aspect, the present invention concerns an isolated antibody which binds a PRO polypeptide. In another aspect, the antibody mimics the activity of a 15 PRO polypeptide (an agonist antibody) or conversely the antibody inhibits or neutralizes the activity of a PRO polypeptide (an antagonist antibody). In another aspect, the antibody is a monoclonal antibody, which preferably has nonhuman complementarity determining region (CDR) residues and human framework region (FR) residues. The antibody may be labeled and may be immobilized on a solid support. In a further aspect, the antibody is an antibody fragment, a monoclonal antibody, a single-chain antibody, or an anti-idiotypic 20 antibody.

In yet another embodiment, the present invention provides a composition comprising an anti-PRO antibody in admixture with a pharmaceutically acceptable carrier. In one aspect, the composition comprises a therapeutically effective amount of the antibody. Preferably, the composition is sterile. The composition may be administered in the form of a liquid pharmaceutical formulation, which may be preserved to achieve 25 extended storage stability. Alternatively, the antibody is a monoclonal antibody, an antibody fragment, a humanized antibody, or a single-chain antibody.

In a further embodiment, the invention concerns an article of manufacture, comprising:

- (a) a composition of matter comprising a PRO polypeptide or agonist or antagonist thereof;
- (b) a container containing said composition; and

30 (c) a label affixed to said container, or a package insert included in said container referring to the use of said PRO polypeptide or agonist or antagonist thereof in the treatment of an immune related disease. The composition may comprise a therapeutically effective amount of the PRO polypeptide or the agonist or antagonist thereof.

In yet another embodiment, the present invention concerns a method of diagnosing an immune 35 related disease in a mammal, comprising detecting the level of expression of a gene encoding a PRO polypeptide (a) in a test sample of tissue cells obtained from the mammal, and (b) in a control sample of known normal tissue cells of the same cell type, wherein a higher or lower expression level in the test sample as compared to the control sample indicates the presence of immune related disease in the mammal from which the test tissue cells were obtained.

40 In another embodiment, the present invention concerns a method of diagnosing an immune disease

in a mammal, comprising (a) contacting an anti-PRO antibody with a test sample of tissue cells obtained from the mammal, and (b) detecting the formation of a complex between the antibody and a PRO polypeptide, in the test sample; wherein the formation of said complex is indicative of the presence or absence of said disease. The detection may be qualitative or quantitative, and may be performed in  
5 comparison with monitoring the complex formation in a control sample of known normal tissue cells of the same cell type. A larger quantity of complexes formed in the test sample indicates the presence or absence of an immune disease in the mammal from which the test tissue cells were obtained. The antibody preferably carries a detectable label. Complex formation can be monitored, for example, by light microscopy, flow cytometry, fluorimetry, or other techniques known in the art. The test sample is usually  
10 obtained from an individual suspected of having a deficiency or abnormality of the immune system.

In another embodiment, the invention provides a method for determining the presence of a PRO polypeptide in a sample comprising exposing a test sample of cells suspected of containing the PRO polypeptide to an anti-PRO antibody and determining the binding of said antibody to said cell sample. In a specific aspect, the sample comprises a cell suspected of containing the PRO polypeptide and the antibody  
15 binds to the cell. The antibody is preferably detectably labeled and/or bound to a solid support.

In another embodiment, the present invention concerns an immune-related disease diagnostic kit, comprising an anti-PRO antibody and a carrier in suitable packaging. The kit preferably contains instructions for using the antibody to detect the presence of the PRO polypeptide. Preferably the carrier is pharmaceutically acceptable.  
20

In another embodiment, the present invention concerns a diagnostic kit, containing an anti-PRO antibody in suitable packaging. The kit preferably contains instructions for using the antibody to detect the PRO polypeptide.  
25

In another embodiment, the invention provides a method of diagnosing an immune-related disease in a mammal which comprises detecting the presence or absence of a PRO polypeptide in a test sample of tissue cells obtained from said mammal, wherein the presence or absence of the PRO polypeptide in said test sample is indicative of the presence of an immune-related disease in said mammal.  
30

In another embodiment, the present invention concerns a method for identifying an agonist of a PRO polypeptide comprising:

(a) contacting cells and a test compound to be screened under conditions suitable for the induction of a cellular response normally induced by a PRO polypeptide; and  
35

(b) determining the induction of said cellular response to determine if the test compound is an effective agonist, wherein the induction of said cellular response is indicative of said test compound being an effective agonist.

In another embodiment, the invention concerns a method for identifying a compound capable of inhibiting the activity of a PRO polypeptide comprising contacting a candidate compound with a PRO polypeptide under conditions and for a time sufficient to allow these two components to interact and determining whether the activity of the PRO polypeptide is inhibited. In a specific aspect, either the candidate compound or the PRO polypeptide is immobilized on a solid support. In another aspect, the non-immobilized component carries a detectable label. In a preferred aspect, this method comprises the steps of:  
40

(a) contacting cells and a test compound to be screened in the presence of a PRO polypeptide under

conditions suitable for the induction of a cellular response normally induced by a PRO polypeptide; and

- (b) determining the induction of said cellular response to determine if the test compound is an effective antagonist.

In another embodiment, the invention provides a method for identifying a compound that inhibits the expression of a PRO polypeptide in cells that normally express the polypeptide, wherein the method comprises contacting the cells with a test compound and determining whether the expression of the PRO polypeptide is inhibited. In a preferred aspect, this method comprises the steps of:

- (a) contacting cells and a test compound to be screened under conditions suitable for allowing expression of the PRO polypeptide; and

- (b) determining the inhibition of expression of said polypeptide.

In yet another embodiment, the present invention concerns a method for treating an immune-related disorder in a mammal that suffers therefrom comprising administering to the mammal a nucleic acid molecule that codes for either (a) a PRO polypeptide, (b) an agonist of a PRO polypeptide or (c) an antagonist of a PRO polypeptide, wherein said agonist or antagonist may be an anti-PRO antibody. In a preferred embodiment, the mammal is human. In another preferred embodiment, the nucleic acid is administered via *ex vivo* gene therapy. In a further preferred embodiment, the nucleic acid is comprised within a vector, more preferably an adenoviral, adeno-associated viral, lentiviral or retroviral vector.

In yet another aspect, the invention provides a recombinant viral particle comprising a viral vector consisting essentially of a promoter, nucleic acid encoding (a) a PRO polypeptide, (b) an agonist polypeptide of a PRO polypeptide, or (c) an antagonist polypeptide of a PRO polypeptide, and a signal sequence for cellular secretion of the polypeptide, wherein the viral vector is in association with viral structural proteins. Preferably, the signal sequence is from a mammal, such as from a native PRO polypeptide.

In a still further embodiment, the invention concerns an *ex vivo* producer cell comprising a nucleic acid construct that expresses retroviral structural proteins and also comprises a retroviral vector consisting essentially of a promoter, nucleic acid encoding (a) a PRO polypeptide, (b) an agonist polypeptide of a PRO polypeptide or (c) an antagonist polypeptide of a PRO polypeptide, and a signal sequence for cellular secretion of the polypeptide, wherein said producer cell packages the retroviral vector in association with the structural proteins to produce recombinant retroviral particles.

In a still further embodiment, the invention provides a method of increasing the activity of T-lymphocytes in a mammal comprising administering to said mammal (a) a PRO polypeptide, (b) an agonist of a PRO polypeptide, or (c) an antagonist of a PRO polypeptide, wherein the activity of T-lymphocytes in the mammal is increased.

In a still further embodiment, the invention provides a method of decreasing the activity of T-lymphocytes in a mammal comprising administering to said mammal (a) a PRO polypeptide, (b) an agonist of a PRO polypeptide, or (c) an antagonist of a PRO polypeptide, wherein the activity of T-lymphocytes in the mammal is decreased.

In a still further embodiment, the invention provides a method of increasing the proliferation of T-lymphocytes in a mammal comprising administering to said mammal (a) a PRO polypeptide, (b) an agonist of a PRO polypeptide, or (c) an antagonist of a PRO polypeptide, wherein the proliferation of T-lymphocytes in the mammal is increased.

In a still further embodiment, the invention provides a method of decreasing the proliferation of T-lymphocytes in a mammal comprising administering to said mammal (a) a PRO polypeptide, (b) an agonist of a PRO polypeptide, or (c) an antagonist of a PRO polypeptide, wherein the proliferation of T-lymphocytes in the mammal is decreased.

5           B.       Additional Embodiments

In other embodiments of the present invention, the invention provides vectors comprising DNA encoding any of the herein described polypeptides. Host cell comprising any such vector are also provided. By way of example, the host cells may be CHO cells, *E. coli*, or yeast. A process for producing any of the herein described polypeptides is further provided and comprises culturing host cells under conditions suitable for expression of the desired polypeptide and recovering the desired polypeptide from the cell culture.

10           In other embodiments, the invention provides chimeric molecules comprising any of the herein described polypeptides fused to a heterologous polypeptide or amino acid sequence. Example of such chimeric molecules comprise any of the herein described polypeptides fused to an epitope tag sequence or a Fc region of an immunoglobulin.

15           In another embodiment, the invention provides an antibody which specifically binds to any of the above or below described polypeptides. Optionally, the antibody is a monoclonal antibody, humanized antibody, antibody fragment or single-chain antibody.

20           In yet other embodiments, the invention provides oligonucleotide probes useful for isolating genomic and cDNA nucleotide sequences or as antisense probes, wherein those probes may be derived from any of the above or below described nucleotide sequences.

25           In other embodiments, the invention provides an isolated nucleic acid molecule comprising a nucleotide sequence that encodes a PRO polypeptide.

30           In one aspect, the isolated nucleic acid molecule comprises a nucleotide sequence having at least about 80% nucleic acid sequence identity, alternatively at least about 81% nucleic acid sequence identity, alternatively at least about 82% nucleic acid sequence identity, alternatively at least about 83% nucleic acid sequence identity, alternatively at least about 84% nucleic acid sequence identity, alternatively at least about 85% nucleic acid sequence identity, alternatively at least about 86% nucleic acid sequence identity, alternatively at least about 87% nucleic acid sequence identity, alternatively at least about 88% nucleic acid sequence identity, alternatively at least about 89% nucleic acid sequence identity, alternatively at least about 90% nucleic acid sequence identity, alternatively at least about 91% nucleic acid sequence identity, alternatively at least about 92% nucleic acid sequence identity, alternatively at least about 93% nucleic acid sequence identity, alternatively at least about 94% nucleic acid sequence identity, alternatively at least about 95% nucleic acid sequence identity, alternatively at least about 96% nucleic acid sequence identity, alternatively at least about 97% nucleic acid sequence identity, alternatively at least about 98% nucleic acid sequence identity and alternatively at least about 99% nucleic acid sequence identity to (a) a DNA molecule encoding a PRO polypeptide having a full-length amino acid sequence as disclosed herein, an amino acid sequence lacking the signal peptide as disclosed herein, an extracellular domain of a transmembrane protein, with or without the signal peptide, as disclosed herein or any other specifically defined fragment of the full-length amino acid sequence as disclosed herein, or (b) the complement of the DNA molecule of (a).

In other aspects, the isolated nucleic acid molecule comprises a nucleotide sequence having at least about 80% nucleic acid sequence identity, alternatively at least about 81% nucleic acid sequence identity, alternatively at least about 82% nucleic acid sequence identity, alternatively at least about 83% nucleic acid sequence identity, alternatively at least about 84% nucleic acid sequence identity, alternatively at least about 85% nucleic acid sequence identity, alternatively at least about 86% nucleic acid sequence identity, alternatively at least about 87% nucleic acid sequence identity, alternatively at least about 88% nucleic acid sequence identity, alternatively at least about 89% nucleic acid sequence identity, alternatively at least about 90% nucleic acid sequence identity, alternatively at least about 91% nucleic acid sequence identity, alternatively at least about 92% nucleic acid sequence identity, alternatively at least about 93% nucleic acid sequence identity, alternatively at least about 94% nucleic acid sequence identity, alternatively at least about 95% nucleic acid sequence identity, alternatively at least about 96% nucleic acid sequence identity, alternatively at least about 97% nucleic acid sequence identity, alternatively at least about 98% nucleic acid sequence identity and alternatively at least about 99% nucleic acid sequence identity to (a) a DNA molecule comprising the coding sequence of a full-length PRO polypeptide cDNA as disclosed herein, the coding sequence of a PRO polypeptide lacking the signal peptide as disclosed herein, the coding sequence of an extracellular domain of a transmembrane PRO polypeptide, with or without the signal peptide, as disclosed herein or the coding sequence of any other specifically defined fragment of the full-length amino acid sequence as disclosed herein, or (b) the complement of the DNA molecule of (a).

In a further aspect, the invention concerns an isolated nucleic acid molecule comprising a nucleotide sequence having at least about 80% nucleic acid sequence identity, alternatively at least about 81% nucleic acid sequence identity, alternatively at least about 82% nucleic acid sequence identity, alternatively at least about 83% nucleic acid sequence identity, alternatively at least about 84% nucleic acid sequence identity, alternatively at least about 85% nucleic acid sequence identity, alternatively at least about 86% nucleic acid sequence identity, alternatively at least about 87% nucleic acid sequence identity, alternatively at least about 88% nucleic acid sequence identity, alternatively at least about 89% nucleic acid sequence identity, alternatively at least about 90% nucleic acid sequence identity, alternatively at least about 91% nucleic acid sequence identity, alternatively at least about 92% nucleic acid sequence identity, alternatively at least about 93% nucleic acid sequence identity, alternatively at least about 94% nucleic acid sequence identity, alternatively at least about 95% nucleic acid sequence identity, alternatively at least about 96% nucleic acid sequence identity, alternatively at least about 97% nucleic acid sequence identity, alternatively at least about 98% nucleic acid sequence identity and alternatively at least about 99% nucleic acid sequence identity to (a) a DNA molecule that encodes the same mature polypeptide encoded by any of the human protein cDNAs as disclosed herein, or (b) the complement of the DNA molecule of (a).

Another aspect the invention provides an isolated nucleic acid molecule comprising a nucleotide sequence encoding a PRO polypeptide which is either transmembrane domain-deleted or transmembrane domain-inactivated, or is complementary to such encoding nucleotide sequence, wherein the transmembrane domain(s) of such polypeptide are disclosed herein. Therefore, soluble extracellular domains of the herein described PRO polypeptides are contemplated.

Another embodiment is directed to fragments of a PRO polypeptide coding sequence, or the complement thereof, that may find use as, for example, hybridization probes, for encoding fragments of a

PRO polypeptide that may optionally encode a polypeptide comprising a binding site for an anti-PRO antibody or as antisense oligonucleotide probes. Such nucleic acid fragments are usually at least about 20 nucleotides in length, alternatively at least about 30 nucleotides in length, alternatively at least about 40 nucleotides in length, alternatively at least about 50 nucleotides in length, alternatively at least about 60  
5 nucleotides in length, alternatively at least about 70 nucleotides in length, alternatively at least about 80 nucleotides in length, alternatively at least about 90 nucleotides in length, alternatively at least about 100 nucleotides in length, alternatively at least about 110 nucleotides in length, alternatively at least about 120 nucleotides in length, alternatively at least about 130 nucleotides in length, alternatively at least about 140 nucleotides in length, alternatively at least about 150 nucleotides in length, alternatively at least about 160  
10 nucleotides in length, alternatively at least about 170 nucleotides in length, alternatively at least about 180 nucleotides in length, alternatively at least about 190 nucleotides in length, alternatively at least about 200 nucleotides in length, alternatively at least about 250 nucleotides in length, alternatively at least about 300 nucleotides in length, alternatively at least about 350 nucleotides in length, alternatively at least about 400 nucleotides in length, alternatively at least about 450 nucleotides in length, alternatively at least about 500  
15 nucleotides in length, alternatively at least about 600 nucleotides in length, alternatively at least about 700 nucleotides in length, alternatively at least about 800 nucleotides in length, alternatively at least about 900 nucleotides in length and alternatively at least about 1000 nucleotides in length, wherein in this context the term "about" means the referenced nucleotide sequence length plus or minus 10% of that referenced length.  
It is noted that novel fragments of a PRO polypeptide-encoding nucleotide sequence may be determined in a  
20 routine manner by aligning the PRO polypeptide-encoding nucleotide sequence with other known nucleotide sequences using any of a number of well known sequence alignment programs and determining which PRO polypeptide-encoding nucleotide sequence fragment(s) are novel. All of such PRO polypeptide-encoding nucleotide sequences are contemplated herein. Also contemplated are the PRO polypeptide fragments encoded by these nucleotide molecule fragments, preferably those PRO polypeptide fragments that comprise  
25 a binding site for an anti-PRO antibody.

In another embodiment, the invention provides isolated PRO polypeptide encoded by any of the isolated nucleic acid sequences herein above identified.

In a certain aspect, the invention concerns an isolated PRO polypeptide, comprising an amino acid sequence having at least about 80% amino acid sequence identity, alternatively at least about 81% amino  
30 acid sequence identity, alternatively at least about 82% amino acid sequence identity, alternatively at least about 83% amino acid sequence identity, alternatively at least about 84% amino acid sequence identity, alternatively at least about 85% amino acid sequence identity, alternatively at least about 86% amino acid sequence identity, alternatively at least about 87% amino acid sequence identity, alternatively at least about 88% amino acid sequence identity, alternatively at least about 89% amino acid sequence identity,  
35 alternatively at least about 90% amino acid sequence identity, alternatively at least about 91% amino acid sequence identity, alternatively at least about 92% amino acid sequence identity, alternatively at least about 93% amino acid sequence identity, alternatively at least about 94% amino acid sequence identity, alternatively at least about 95% amino acid sequence identity, alternatively at least about 96% amino acid sequence identity, alternatively at least about 97% amino acid sequence identity, alternatively at least about 98% amino acid sequence identity and alternatively at least about 99% amino acid sequence identity to a  
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PRO polypeptide having a full-length amino acid sequence as disclosed herein, an amino acid sequence lacking the signal peptide as disclosed herein, an extracellular domain of a transmembrane protein, with or without the signal peptide, as disclosed herein or any other specifically defined fragment of the full-length amino acid sequence as disclosed herein.

5 In a further aspect, the invention concerns an isolated PRO polypeptide comprising an amino acid sequence having at least about 80% amino acid sequence identity, alternatively at least about 81% amino acid sequence identity, alternatively at least about 82% amino acid sequence identity, alternatively at least about 83% amino acid sequence identity, alternatively at least about 84% amino acid sequence identity, alternatively at least about 85% amino acid sequence identity, alternatively at least about 86% amino acid  
10 sequence identity, alternatively at least about 87% amino acid sequence identity, alternatively at least about 88% amino acid sequence identity, alternatively at least about 89% amino acid sequence identity, alternatively at least about 90% amino acid sequence identity, alternatively at least about 91% amino acid sequence identity, alternatively at least about 92% amino acid sequence identity, alternatively at least about 93% amino acid sequence identity, alternatively at least about 94% amino acid sequence identity,  
15 alternatively at least about 95% amino acid sequence identity, alternatively at least about 96% amino acid sequence identity, alternatively at least about 97% amino acid sequence identity, alternatively at least about 98% amino acid sequence identity and alternatively at least about 99% amino acid sequence identity to an amino acid sequence encoded by any of the human protein cDNAs as disclosed herein.

In a specific aspect, the invention provides an isolated PRO polypeptide without the N-terminal  
20 signal sequence and/or the initiating methionine and is encoded by a nucleotide sequence that encodes such an amino acid sequence as herein before described. Processes for producing the same are also herein described, wherein those processes comprise culturing a host cell comprising a vector which comprises the appropriate encoding nucleic acid molecule under conditions suitable for expression of the PRO polypeptide and recovering the PRO polypeptide from the cell culture.

25 Another aspect the invention provides an isolated PRO polypeptide which is either transmembrane domain-deleted or transmembrane domain-inactivated. Processes for producing the same are also herein described, wherein those processes comprise culturing a host cell comprising a vector which comprises the appropriate encoding nucleic acid molecule under conditions suitable for expression of the PRO polypeptide and recovering the PRO polypeptide from the cell culture.

30 In yet another embodiment, the invention concerns agonists and antagonists of a native PRO polypeptide as defined herein. In a particular embodiment, the agonist or antagonist is an anti-PRO antibody or a small molecule.

In a further embodiment, the invention concerns a method of identifying agonists or antagonists to a  
35 PRO polypeptide which comprise contacting the PRO polypeptide with a candidate molecule and monitoring a biological activity mediated by said PRO polypeptide. Preferably, the PRO polypeptide is a native PRO polypeptide.

In a still further embodiment, the invention concerns a composition of matter comprising a PRO polypeptide, or an agonist or antagonist of a PRO polypeptide as herein described, or an anti-PRO antibody, in combination with a carrier. Optionally, the carrier is a pharmaceutically acceptable carrier.

40 Another embodiment of the present invention is directed to the use of a PRO polypeptide, or an

agonist or antagonist thereof as herein before described, or an anti-PRO antibody, for the preparation of a medicament useful in the treatment of a condition which is responsive to the PRO polypeptide, an agonist or antagonist thereof or an anti-PRO antibody.

5

#### BRIEF DESCRIPTION OF THE DRAWINGS

SEQ ID NOS 1-6464 show the nucleic acids of the invention and their encoded PRO polypeptides. Also included, for convenience is a List of Figures attached hereto as Appendix A, in which each Figure number corresponds to the same number SEQ ID NO: in the sequence listing. For example, Figure 1 equals SEQ ID NO:1 of the sequence listing.

10

#### DETAILED DESCRIPTION OF THE PREFERRED EMBODIMENTS

##### I. Definitions

The terms "PRO polypeptide" and "PRO" as used herein and when immediately followed by a numerical designation refer to various polypeptides, wherein the complete designation (i.e., PRO/number) refers to specific polypeptide sequences as described herein. The terms "PRO/number polypeptide" and "PRO/number" wherein the term "number" is provided as an actual numerical designation as used herein encompass native sequence polypeptides and polypeptide variants (which are further defined herein). The PRO polypeptides described herein may be isolated from a variety of sources, such as from human tissue types or from another source, or prepared by recombinant or synthetic methods. The term "PRO polypeptide" refers to each individual PRO/number polypeptide disclosed herein. All disclosures in this specification which refer to the "PRO polypeptide" refer to each of the polypeptides individually as well as jointly. For example, descriptions of the preparation of, purification of, derivation of, formation of antibodies to or against, administration of, compositions containing, treatment of a disease with, etc., pertain to each polypeptide of the invention individually. The term "PRO polypeptide" also includes variants of the PRO/number polypeptides disclosed herein.

A "native sequence PRO polypeptide" comprises a polypeptide having the same amino acid sequence as the corresponding PRO polypeptide derived from nature. Such native sequence PRO polypeptides can be isolated from nature or can be produced by recombinant or synthetic means. The term "native sequence PRO polypeptide" specifically encompasses naturally-occurring truncated or secreted forms of the specific PRO polypeptide (e.g., an extracellular domain sequence), naturally-occurring variant forms (e.g., alternatively spliced forms) and naturally-occurring allelic variants of the polypeptide. In various embodiments of the invention, the native sequence PRO polypeptides disclosed herein are mature or full-length native sequence polypeptides comprising the full-length amino acids sequences shown in the accompanying figures. Start and stop codons are shown in bold font and underlined in the figures.

However, while the PRO polypeptide disclosed in the accompanying figures are shown to begin with methionine residues designated herein as amino acid position 1 in the figures, it is conceivable and possible that other methionine residues located either upstream or downstream from the amino acid position 1 in the figures may be employed as the starting amino acid residue for the PRO polypeptides.

The PRO polypeptide "extracellular domain" or "ECD" refers to a form of the PRO polypeptide which is essentially free of the transmembrane and cytoplasmic domains. Ordinarily, a PRO polypeptide

ECD will have less than 1% of such transmembrane and/or cytoplasmic domains and preferably, will have less than 0.5% of such domains. It will be understood that any transmembrane domains identified for the PRO polypeptides of the present invention are identified pursuant to criteria routinely employed in the art for identifying that type of hydrophobic domain. The exact boundaries of a transmembrane domain may vary 5 but most likely by no more than about 5 amino acids at either end of the domain as initially identified herein. Optionally, therefore, an extracellular domain of a PRO polypeptide may contain from about 5 or fewer amino acids on either side of the transmembrane domain/extracellular domain boundary as identified in the Examples or specification and such polypeptides, with or without the associated signal peptide, and nucleic acid encoding them, are contemplated by the present invention.

10 The approximate location of the "signal peptides" of the various PRO polypeptides disclosed herein are shown in the present specification and/or the accompanying figures. It is noted, however, that the C-terminal boundary of a signal peptide may vary, but most likely by no more than about 5 amino acids on either side of the signal peptide C-terminal boundary as initially identified herein, wherein the C-terminal boundary of the signal peptide may be identified pursuant to criteria routinely employed in the art for 15 identifying that type of amino acid sequence element (e.g., Nielsen et al., Prot. Eng. 10:1-6 (1997) and von Heinje et al., Nucl. Acids. Res. 14:4683-4690 (1986)). Moreover, it is also recognized that, in some cases, cleavage of a signal sequence from a secreted polypeptide is not entirely uniform, resulting in more than one secreted species. These mature polypeptides, where the signal peptide is cleaved within no more than about 5 amino acids on either side of the C-terminal boundary of the signal peptide as identified herein, and the 20 polynucleotides encoding them, are contemplated by the present invention.

"PRO polypeptide variant" means an active PRO polypeptide as defined above or below having at least about 80% amino acid sequence identity with a full-length native sequence PRO polypeptide sequence as disclosed herein, a PRO polypeptide sequence lacking the signal peptide as disclosed herein, an extracellular domain of a PRO polypeptide, with or without the signal peptide, as disclosed herein or any 25 other fragment of a full-length PRO polypeptide sequence as disclosed herein. Such PRO polypeptide variants include, for instance, PRO polypeptides wherein one or more amino acid residues are added, or deleted, at the N- or C-terminus of the full-length native amino acid sequence. Ordinarily, a PRO polypeptide variant will have at least about 80% amino acid sequence identity, alternatively at least about 81% amino acid sequence identity, alternatively at least about 82% amino acid sequence identity, 30 alternatively at least about 83% amino acid sequence identity, alternatively at least about 84% amino acid sequence identity, alternatively at least about 85% amino acid sequence identity, alternatively at least about 86% amino acid sequence identity, alternatively at least about 87% amino acid sequence identity, alternatively at least about 88% amino acid sequence identity, alternatively at least about 89% amino acid sequence identity, alternatively at least about 90% amino acid sequence identity, alternatively at least about 35 91% amino acid sequence identity, alternatively at least about 92% amino acid sequence identity, alternatively at least about 93% amino acid sequence identity, alternatively at least about 94% amino acid sequence identity, alternatively at least about 95% amino acid sequence identity, alternatively at least about 96% amino acid sequence identity, alternatively at least about 97% amino acid sequence identity, alternatively at least about 98% amino acid sequence identity and alternatively at least about 99% amino 40 acid sequence identity to a full-length native sequence PRO polypeptide sequence as disclosed herein, a

PRO polypeptide sequence lacking the signal peptide as disclosed herein, an extracellular domain of a PRO polypeptide, with or without the signal peptide, as disclosed herein or any other specifically defined fragment of a full-length PRO polypeptide sequence as disclosed herein. Ordinarily, PRO variant polypeptides are at least about 10 amino acids in length, alternatively at least about 20 amino acids in length, 5 alternatively at least about 30 amino acids in length, alternatively at least about 40 amino acids in length, alternatively at least about 50 amino acids in length, alternatively at least about 60 amino acids in length, alternatively at least about 70 amino acids in length, alternatively at least about 80 amino acids in length, alternatively at least about 90 amino acids in length, alternatively at least about 100 amino acids in length, alternatively at least about 150 amino acids in length, alternatively at least about 200 amino acids in length, 10 alternatively at least about 300 amino acids in length, or more.

"Percent (%) amino acid sequence identity" with respect to the PRO polypeptide sequences identified herein is defined as the percentage of amino acid residues in a candidate sequence that are identical with the amino acid residues in the specific PRO polypeptide sequence, after aligning the sequences and introducing gaps, if necessary, to achieve the maximum percent sequence identity, and not 15 considering any conservative substitutions as part of the sequence identity. Alignment for purposes of determining percent amino acid sequence identity can be achieved in various ways that are within the skill in the art, for instance, using publicly available computer software such as BLAST, BLAST-2, ALIGN or Megalign (DNASTAR) software. Those skilled in the art can determine appropriate parameters for measuring alignment, including any algorithms needed to achieve maximal alignment over the full length of 20 the sequences being compared. For purposes herein, however, % amino acid sequence identity values are generated using the sequence comparison computer program ALIGN-2, wherein the complete source code for the ALIGN-2 program is provided in Table 1 below. The ALIGN-2 sequence comparison computer program was authored by Genentech, Inc. and the source code shown in Table 1 below has been filed with user documentation in the U.S. Copyright Office, Washington D.C., 20559, where it is registered under U.S. 25 Copyright Registration No. TXU510087. The ALIGN-2 program is publicly available through Genentech, Inc., South San Francisco, California or may be compiled from the source code provided in Table 1 below. The ALIGN-2 program should be compiled for use on a UNIX operating system, preferably digital UNIX V4.0D. All sequence comparison parameters are set by the ALIGN-2 program and do not vary.

In situations where ALIGN-2 is employed for amino acid sequence comparisons, the % amino acid 30 sequence identity of a given amino acid sequence A to, with, or against a given amino acid sequence B (which can alternatively be phrased as a given amino acid sequence A that has or comprises a certain % amino acid sequence identity to, with, or against a given amino acid sequence B) is calculated as follows:

$$100 \text{ times the fraction } X/Y$$

35 where X is the number of amino acid residues scored as identical matches by the sequence alignment program ALIGN-2 in that program's alignment of A and B, and where Y is the total number of amino acid residues in B. It will be appreciated that where the length of amino acid sequence A is not equal to the length of amino acid sequence B, the % amino acid sequence identity of A to B will not equal the % amino 40 acid sequence identity of B to A. As examples of % amino acid sequence identity calculations using this

method, Tables 2 and 3 demonstrate how to calculate the % amino acid sequence identity of the amino acid sequence designated "Comparison Protein" to the amino acid sequence designated "PRO", wherein "PRO" represents the amino acid sequence of a hypothetical PRO polypeptide of interest, "Comparison Protein" represents the amino acid sequence of a polypeptide against which the "PRO" polypeptide of interest is being compared, and "X, "Y" and "Z" each represent different hypothetical amino acid residues.

Unless specifically stated otherwise, all % amino acid sequence identity values used herein are obtained as described in the immediately preceding paragraph using the ALIGN-2 computer program. However, % amino acid sequence identity values may also be obtained as described below by using the WU-BLAST-2 computer program (Altschul et al., Methods in Enzymology 266:460-480 (1996)). Most of the WU-BLAST-2 search parameters are set to the default values. Those not set to default values, i.e., the adjustable parameters, are set with the following values: overlap span = 1, overlap fraction = 0.125, word threshold (T) = 11, and scoring matrix = BLOSUM62. When WU-BLAST-2 is employed, a % amino acid sequence identity value is determined by dividing (a) the number of matching identical amino acid residues between the amino acid sequence of the PRO polypeptide of interest having a sequence derived from the native PRO polypeptide and the comparison amino acid sequence of interest (i.e., the sequence against which the PRO polypeptide of interest is being compared which may be a PRO variant polypeptide) as determined by WU-BLAST-2 by (b) the total number of amino acid residues of the PRO polypeptide of interest. For example, in the statement "a polypeptide comprising an the amino acid sequence A which has or having at least 80% amino acid sequence identity to the amino acid sequence B", the amino acid sequence A is the comparison amino acid sequence of interest and the amino acid sequence B is the amino acid sequence of the PRO polypeptide of interest.

Percent amino acid sequence identity may also be determined using the sequence comparison program NCBI-BLAST2 (Altschul et al., Nucleic Acids Res. 25:3389-3402 (1997)). The NCBI-BLAST2 sequence comparison program may be downloaded from <http://www.ncbi.nlm.nih.gov> or otherwise obtained from the National Institute of Health, Bethesda, MD. NCBI-BLAST2 uses several search parameters, wherein all of those search parameters are set to default values including, for example, unmask = yes, strand = all, expected occurrences = 10, minimum low complexity length = 15/5, multi-pass e-value = 0.01, constant for multi-pass = 25, dropoff for final gapped alignment = 25 and scoring matrix = BLOSUM62.

In situations where NCBI-BLAST2 is employed for amino acid sequence comparisons, the % amino acid sequence identity of a given amino acid sequence A to, with, or against a given amino acid sequence B (which can alternatively be phrased as a given amino acid sequence A that has or comprises a certain % amino acid sequence identity to, with, or against a given amino acid sequence B) is calculated as follows:

35

100 times the fraction X/Y

where X is the number of amino acid residues scored as identical matches by the sequence alignment program NCBI-BLAST2 in that program's alignment of A and B, and where Y is the total number of amino acid residues in B. It will be appreciated that where the length of amino acid sequence A is not equal to the

length of amino acid sequence B, the % amino acid sequence identity of A to B will not equal the % amino acid sequence identity of B to A.

"PRO variant polynucleotide" or "PRO variant nucleic acid sequence" means a nucleic acid molecule which encodes an active PRO polypeptide as defined below and which has at least about 80% nucleic acid sequence identity with a nucleotide acid sequence encoding a full-length native sequence PRO polypeptide sequence as disclosed herein, a full-length native sequence PRO polypeptide sequence lacking the signal peptide as disclosed herein, an extracellular domain of a PRO polypeptide, with or without the signal peptide, as disclosed herein or any other fragment of a full-length PRO polypeptide sequence as disclosed herein. Ordinarily, a PRO variant polynucleotide will have at least about 80% nucleic acid sequence identity, alternatively at least about 81% nucleic acid sequence identity, alternatively at least about 82% nucleic acid sequence identity, alternatively at least about 83% nucleic acid sequence identity, alternatively at least about 84% nucleic acid sequence identity, alternatively at least about 85% nucleic acid sequence identity, alternatively at least about 86% nucleic acid sequence identity, alternatively at least about 87% nucleic acid sequence identity, alternatively at least about 88% nucleic acid sequence identity, alternatively at least about 89% nucleic acid sequence identity, alternatively at least about 90% nucleic acid sequence identity, alternatively at least about 91% nucleic acid sequence identity, alternatively at least about 92% nucleic acid sequence identity, alternatively at least about 93% nucleic acid sequence identity, alternatively at least about 94% nucleic acid sequence identity, alternatively at least about 95% nucleic acid sequence identity, alternatively at least about 96% nucleic acid sequence identity, alternatively at least about 97% nucleic acid sequence identity, alternatively at least about 98% nucleic acid sequence identity and alternatively at least about 99% nucleic acid sequence identity with a nucleic acid sequence encoding a full-length native sequence PRO polypeptide sequence as disclosed herein, a full-length native sequence PRO polypeptide sequence lacking the signal peptide as disclosed herein, an extracellular domain of a PRO polypeptide, with or without the signal sequence, as disclosed herein or any other fragment of a full-length PRO polypeptide sequence as disclosed herein. Variants do not encompass the native nucleotide sequence.

Ordinarily, PRO variant polynucleotides are at least about 30 nucleotides in length, alternatively at least about 60 nucleotides in length, alternatively at least about 90 nucleotides in length, alternatively at least about 120 nucleotides in length, alternatively at least about 150 nucleotides in length, alternatively at least about 180 nucleotides in length, alternatively at least about 210 nucleotides in length, alternatively at least about 240 nucleotides in length, alternatively at least about 270 nucleotides in length, alternatively at least about 300 nucleotides in length, alternatively at least about 450 nucleotides in length, alternatively at least about 600 nucleotides in length, alternatively at least about 900 nucleotides in length, or more.

"Percent (%) nucleic acid sequence identity" with respect to PRO-encoding nucleic acid sequences identified herein is defined as the percentage of nucleotides in a candidate sequence that are identical with the nucleotides in the PRO nucleic acid sequence of interest, after aligning the sequences and introducing gaps, if necessary, to achieve the maximum percent sequence identity. Alignment for purposes of determining percent nucleic acid sequence identity can be achieved in various ways that are within the skill in the art, for instance, using publicly available computer software such as BLAST, BLAST-2, ALIGN or Megalign (DNASTAR) software. For purposes herein, however, % nucleic acid sequence identity values are generated using the sequence comparison computer program ALIGN-2, wherein the complete source code

for the ALIGN-2 program is provided in Table 1 below. The ALIGN-2 sequence comparison computer program was authored by Genentech, Inc. and the source code shown in Table 1 below has been filed with user documentation in the U.S. Copyright Office, Washington D.C., 20559, where it is registered under U.S. Copyright Registration No. TXU510087. The ALIGN-2 program is publicly available through Genentech, Inc., South San Francisco, California or may be compiled from the source code provided in Table 1 below. The ALIGN-2 program should be compiled for use on a UNIX operating system, preferably digital UNIX V4.0D. All sequence comparison parameters are set by the ALIGN-2 program and do not vary.

In situations where ALIGN-2 is employed for nucleic acid sequence comparisons, the % nucleic acid sequence identity of a given nucleic acid sequence C to, with, or against a given nucleic acid sequence D (which can alternatively be phrased as a given nucleic acid sequence C that has or comprises a certain % nucleic acid sequence identity to, with, or against a given nucleic acid sequence D) is calculated as follows:

$$100 \text{ times the fraction } W/Z$$

where W is the number of nucleotides scored as identical matches by the sequence alignment program ALIGN-2 in that program's alignment of C and D, and where Z is the total number of nucleotides in D. It will be appreciated that where the length of nucleic acid sequence C is not equal to the length of nucleic acid sequence D, the % nucleic acid sequence identity of C to D will not equal the % nucleic acid sequence identity of D to C. As examples of % nucleic acid sequence identity calculations, Tables 4 and 5, demonstrate how to calculate the % nucleic acid sequence identity of the nucleic acid sequence designated "Comparison DNA" to the nucleic acid sequence designated "PRO-DNA", wherein "PRO-DNA" represents a hypothetical PRO-encoding nucleic acid sequence of interest, "Comparison DNA" represents the nucleotide sequence of a nucleic acid molecule against which the "PRO-DNA" nucleic acid molecule of interest is being compared, and "N", "L" and "V" each represent different hypothetical nucleotides.

Unless specifically stated otherwise, all % nucleic acid sequence identity values used herein are obtained as described in the immediately preceding paragraph using the ALIGN-2 computer program. However, % nucleic acid sequence identity values may also be obtained as described below by using the WU-BLAST-2 computer program (Altschul et al., *Methods in Enzymology* 266:460-480 (1996)). Most of the WU-BLAST-2 search parameters are set to the default values. Those not set to default values, i.e., the adjustable parameters, are set with the following values: overlap span = 1, overlap fraction = 0.125, word threshold (T) = 11, and scoring matrix = BLOSUM62. When WU-BLAST-2 is employed, a % nucleic acid sequence identity value is determined by dividing (a) the number of matching identical nucleotides between the nucleic acid sequence of the PRO polypeptide-encoding nucleic acid molecule of interest having a sequence derived from the native sequence PRO polypeptide-encoding nucleic acid and the comparison nucleic acid molecule of interest (i.e., the sequence against which the PRO polypeptide-encoding nucleic acid molecule of interest is being compared which may be a variant PRO polynucleotide) as determined by WU-BLAST-2 by (b) the total number of nucleotides of the PRO polypeptide-encoding nucleic acid molecule of interest. For example, in the statement "an isolated nucleic acid molecule comprising a nucleic acid sequence A which has or having at least 80% nucleic acid sequence identity to the nucleic acid sequence B", the nucleic acid sequence A is the comparison nucleic acid molecule of interest and the nucleic

acid sequence B is the nucleic acid sequence of the PRO polypeptide-encoding nucleic acid molecule of interest

Percent nucleic acid sequence identity may also be determined using the sequence comparison program NCBI-BLAST2 (Altschul et al., *Nucleic Acids Res.* 25:3389-3402 (1997)). The NCBI-BLAST2 sequence comparison program may be downloaded from <http://www.ncbi.nlm.nih.gov> or otherwise obtained from the National Institute of Health, Bethesda, MD. NCBI-BLAST2 uses several search parameters, wherein all of those search parameters are set to default values including, for example, unmask = yes, strand = all, expected occurrences = 10, minimum low complexity length = 15/5, multi-pass e-value = 0.01, constant for multi-pass = 25, dropoff for final gapped alignment = 25 and scoring matrix = BLOSUM62.

10 In situations where NCBI-BLAST2 is employed for sequence comparisons, the % nucleic acid sequence identity of a given nucleic acid sequence C to, with, or against a given nucleic acid sequence D (which can alternatively be phrased as a given nucleic acid sequence C that has or comprises a certain % nucleic acid sequence identity to, with, or against a given nucleic acid sequence D) is calculated as follows:

15 100 times the fraction W/Z

where W is the number of nucleotides scored as identical matches by the sequence alignment program NCBI-BLAST2 in that program's alignment of C and D, and where Z is the total number of nucleotides in D. It will be appreciated that where the length of nucleic acid sequence C is not equal to the length of nucleic acid sequence D, the % nucleic acid sequence identity of C to D will not equal the % nucleic acid sequence identity of D to C.

In other embodiments, PRO variant polynucleotides are nucleic acid molecules that encode an active PRO polypeptide and which are capable of hybridizing, preferably under stringent hybridization and wash conditions, to nucleotide sequences encoding a full-length PRO polypeptide as disclosed herein. PRO variant polypeptides may be those that are encoded by a PRO variant polynucleotide.

"Isolated," when used to describe the various polypeptides disclosed herein, means polypeptide that has been identified and separated and/or recovered from a component of its natural environment. Contaminant components of its natural environment are materials that would typically interfere with diagnostic or therapeutic uses for the polypeptide, and may include enzymes, hormones, and other proteinaceous or non-proteinaceous solutes. In preferred embodiments, the polypeptide will be purified (1) to a degree sufficient to obtain at least 15 residues of N-terminal or internal amino acid sequence by use of a spinning cup sequenator, or (2) to homogeneity by SDS-PAGE under non-reducing or reducing conditions using Coomassie blue or, preferably, silver stain. Isolated polypeptide includes polypeptide *in situ* within recombinant cells, since at least one component of the PRO polypeptide natural environment will not be present. Ordinarily, however, isolated polypeptide will be prepared by at least one purification step.

An "isolated" PRO polypeptide-encoding nucleic acid or other polypeptide-encoding nucleic acid is a nucleic acid molecule that is identified and separated from at least one contaminant nucleic acid molecule with which it is ordinarily associated in the natural source of the polypeptide-encoding nucleic acid. An isolated polypeptide-encoding nucleic acid molecule is other than in the form or setting in which it is found in nature. Isolated polypeptide-encoding nucleic acid molecules therefore are distinguished from the

specific polypeptide-encoding nucleic acid molecule as it exists in natural cells. However, an isolated polypeptide-encoding nucleic acid molecule includes polypeptide-encoding nucleic acid molecules contained in cells that ordinarily express the polypeptide where, for example, the nucleic acid molecule is in a chromosomal location different from that of natural cells.

5       The term "control sequences" refers to DNA sequences necessary for the expression of an operably linked coding sequence in a particular host organism. The control sequences that are suitable for prokaryotes, for example, include a promoter, optionally an operator sequence, and a ribosome binding site. Eukaryotic cells are known to utilize promoters, polyadenylation signals, and enhancers.

Nucleic acid is "operably linked" when it is placed into a functional relationship with another 10 nucleic acid sequence. For example, DNA for a presequence or secretory leader is operably linked to DNA for a polypeptide if it is expressed as a preprotein that participates in the secretion of the polypeptide; a promoter or enhancer is operably linked to a coding sequence if it affects the transcription of the sequence; or a ribosome binding site is operably linked to a coding sequence if it is positioned so as to facilitate 15 translation. Generally, "operably linked" means that the DNA sequences being linked are contiguous, and, in the case of a secretory leader, contiguous and in reading phase. However, enhancers do not have to be contiguous. Linking is accomplished by ligation at convenient restriction sites. If such sites do not exist, the synthetic oligonucleotide adaptors or linkers are used in accordance with conventional practice.

The term "antibody" is used in the broadest sense and specifically covers, for example, single anti-PRO monoclonal antibodies (including agonist, antagonist, and neutralizing antibodies), anti-PRO antibody 20 compositions with polyepitopic specificity, single chain anti-PRO antibodies, and fragments of anti-PRO antibodies (see below). The term "monoclonal antibody" as used herein refers to an antibody obtained from a population of substantially homogeneous antibodies, i.e., the individual antibodies comprising the population are identical except for possible naturally-occurring mutations that may be present in minor amounts.

25       "Stringency" of hybridization reactions is readily determinable by one of ordinary skill in the art, and generally is an empirical calculation dependent upon probe length, washing temperature, and salt concentration. In general, longer probes require higher temperatures for proper annealing, while shorter probes need lower temperatures. Hybridization generally depends on the ability of denatured DNA to reanneal when complementary strands are present in an environment below their melting temperature. The 30 higher the degree of desired homology between the probe and hybridizable sequence, the higher the relative temperature which can be used. As a result, it follows that higher relative temperatures would tend to make the reaction conditions more stringent, while lower temperatures less so. For additional details and explanation of stringency of hybridization reactions, see Ausubel et al., Current Protocols in Molecular Biology, Wiley Interscience Publishers, (1995).

35       "Stringent conditions" or "high stringency conditions", as defined herein, may be identified by those that: (1) employ low ionic strength and high temperature for washing, for example 0.015 M sodium chloride/0.0015 M sodium citrate/0.1% sodium dodecyl sulfate at 50°C; (2) employ during hybridization a denaturing agent, such as formamide, for example, 50% (v/v) formamide with 0.1% bovine serum albumin/0.1% Ficoll/0.1% polyvinylpyrrolidone/50mM sodium phosphate buffer at pH 6.5 with 750 mM 40 sodium chloride, 75 mM sodium citrate at 42°C; or (3) employ 50% formamide, 5 x SSC (0.75 M NaCl,

0.075 M sodium citrate), 50 mM sodium phosphate (pH 6.8), 0.1% sodium pyrophosphate, 5 x Denhardt's solution, sonicated salmon sperm DNA (50 µg/ml), 0.1% SDS, and 10% dextran sulfate at 42°C, with washes at 42°C in 0.2 x SSC (sodium chloride/sodium citrate) and 50% formamide at 55°C, followed by a high-stringency wash consisting of 0.1 x SSC containing EDTA at 55°C.

5 "Moderately stringent conditions" may be identified as described by Sambrook et al., Molecular Cloning: A Laboratory Manual, New York: Cold Spring Harbor Press, 1989, and include the use of washing solution and hybridization conditions (e.g., temperature, ionic strength and %SDS) less stringent than those described above. An example of moderately stringent conditions is overnight incubation at 37°C in a solution comprising: 20% formamide, 5 x SSC (150 mM NaCl, 15 mM trisodium citrate), 50 mM sodium 10 phosphate (pH 7.6), 5 x Denhardt's solution, 10% dextran sulfate, and 20 mg/ml denatured sheared salmon sperm DNA, followed by washing the filters in 1 x SSC at about 37-50°C. The skilled artisan will recognize how to adjust the temperature, ionic strength, etc. as necessary to accommodate factors such as probe length 15 and the like.

The term "epitope tagged" when used herein refers to a chimeric polypeptide comprising a PRO 15 polypeptide fused to a "tag polypeptide". The tag polypeptide has enough residues to provide an epitope against which an antibody can be made, yet is short enough such that it does not interfere with activity of the polypeptide to which it is fused. The tag polypeptide preferably also is fairly unique so that the antibody does not substantially cross-react with other epitopes. Suitable tag polypeptides generally have at least six 20 amino acid residues and usually between about 8 and 50 amino acid residues (preferably, between about 10 and 20 amino acid residues).

As used herein, the term "immunoadhesin" designates antibody-like molecules which combine the binding specificity of a heterologous protein (an "adhesin") with the effector functions of immunoglobulin constant domains. Structurally, the immunoadhesins comprise a fusion of an amino acid sequence with the desired binding specificity which is other than the antigen recognition and binding site of an antibody (i.e., is 25 "heterologous"), and an immunoglobulin constant domain sequence. The adhesin part of an immunoadhesin molecule typically is a contiguous amino acid sequence comprising at least the binding site of a receptor or a ligand. The immunoglobulin constant domain sequence in the immunoadhesin may be obtained from any immunoglobulin, such as IgG-1, IgG-2, IgG-3, or IgG-4 subtypes, IgA (including IgA-1 and IgA-2), IgE, IgD or IgM.

30 "Active" or "activity" for the purposes herein refers to form(s) of a PRO polypeptide which retain a biological and/or an immunological activity of native or naturally-occurring PRO, wherein "biological" activity refers to a biological function (either inhibitory or stimulatory) caused by a native or naturally-occurring PRO other than the ability to induce the production of an antibody against an antigenic epitope possessed by a native or naturally-occurring PRO and an "immunological" activity refers to the ability to 35 induce the production of an antibody against an antigenic epitope possessed by a native or naturally-occurring PRO.

The term "antagonist" is used in the broadest sense, and includes any molecule that partially or fully blocks, inhibits, or neutralizes a biological activity of a native PRO polypeptide disclosed herein. In a similar manner, the term "agonist" is used in the broadest sense and includes any molecule that mimics a 40 biological activity of a native PRO polypeptide disclosed herein. Suitable agonist or antagonist molecules

specifically include agonist or antagonist antibodies or antibody fragments, fragments or amino acid sequence variants of native PRO polypeptides, peptides, antisense oligonucleotides, small organic molecules, etc. Methods for identifying agonists or antagonists of a PRO polypeptide may comprise contacting a PRO polypeptide with a candidate agonist or antagonist molecule and measuring a detectable change in one or more biological activities normally associated with the PRO polypeptide.

"Treatment" refers to both therapeutic treatment and prophylactic or preventative measures, wherein the object is to prevent or slow down (lessen) the targeted pathologic condition or disorder. Those in need of treatment include those already with the disorder as well as those prone to have the disorder or those in whom the disorder is to be prevented.

"Chronic" administration refers to administration of the agent(s) in a continuous mode as opposed to an acute mode, so as to maintain the initial therapeutic effect (activity) for an extended period of time. "Intermittent" administration is treatment that is not consecutively done without interruption, but rather is cyclic in nature.

"Mammal" for purposes of treatment refers to any animal classified as a mammal, including humans, domestic and farm animals, and zoo, sports, or pet animals, such as dogs, cats, cattle, horses, sheep, pigs, goats, rabbits, etc. Preferably, the mammal is human.

Administration "in combination with" one or more further therapeutic agents includes simultaneous (concurrent) and consecutive administration in any order.

"Carriers" as used herein include pharmaceutically acceptable carriers, excipients, or stabilizers which are nontoxic to the cell or mammal being exposed thereto at the dosages and concentrations employed. Often the physiologically acceptable carrier is an aqueous pH buffered solution. Examples of physiologically acceptable carriers include buffers such as phosphate, citrate, and other organic acids; antioxidants including ascorbic acid; low molecular weight (less than about 10 residues) polypeptide; proteins, such as serum albumin, gelatin, or immunoglobulins; hydrophilic polymers such as polyvinylpyrrolidone; amino acids such as glycine, glutamine, asparagine, arginine or lysine; monosaccharides, disaccharides, and other carbohydrates including glucose, mannose, or dextrins; chelating agents such as EDTA; sugar alcohols such as mannitol or sorbitol; salt-forming counterions such as sodium; and/or nonionic surfactants such as TWEEN™, polyethylene glycol (PEG), and PLURONICS™.

"Antibody fragments" comprise a portion of an intact antibody, preferably the antigen binding or variable region of the intact antibody. Examples of antibody fragments include Fab, Fab', F(ab')<sub>2</sub>, and Fv fragments; diabodies; linear antibodies (Zapata et al., *Protein Eng.* 8(10): 1057-1062 [1995]); single-chain antibody molecules; and multispecific antibodies formed from antibody fragments.

Papain digestion of antibodies produces two identical antigen-binding fragments, called "Fab" fragments, each with a single antigen-binding site, and a residual "Fc" fragment, a designation reflecting the ability to crystallize readily. Pepsin treatment yields an F(ab')<sub>2</sub> fragment that has two antigen-combining sites and is still capable of cross-linking antigen.

"Fv" is the minimum antibody fragment which contains a complete antigen-recognition and - binding site. This region consists of a dimer of one heavy- and one light-chain variable domain in tight, non-covalent association. It is in this configuration that the three CDRs of each variable domain interact to define an antigen-binding site on the surface of the V<sub>H</sub>-V<sub>L</sub> dimer. Collectively, the six CDRs confer antigen-

binding specificity to the antibody. However, even a single variable domain (or half of an Fv comprising only three CDRs specific for an antigen) has the ability to recognize and bind antigen, although at a lower affinity than the entire binding site.

The Fab fragment also contains the constant domain of the light chain and the first constant domain (CH1) of the heavy chain. Fab fragments differ from Fab' fragments by the addition of a few residues at the carboxy terminus of the heavy chain CH1 domain including one or more cysteines from the antibody hinge region. Fab'-SH is the designation herein for Fab' in which the cysteine residue(s) of the constant domains bear a free thiol group. F(ab')<sub>2</sub> antibody fragments originally were produced as pairs of Fab' fragments which have hinge cysteines between them. Other chemical couplings of antibody fragments are also known.

10 The "light chains" of antibodies (immunoglobulins) from any vertebrate species can be assigned to one of two clearly distinct types, called kappa and lambda, based on the amino acid sequences of their constant domains.

Depending on the amino acid sequence of the constant domain of their heavy chains, immunoglobulins can be assigned to different classes. There are five major classes of immunoglobulins: 15 IgA, IgD, IgE, IgG, and IgM, and several of these may be further divided into subclasses (isotypes), e.g., IgG1, IgG2, IgG3, IgG4, IgA, and IgA2.

"Single-chain Fv" or "sFv" antibody fragments comprise the V<sub>H</sub> and V<sub>L</sub> domains of antibody, wherein these domains are present in a single polypeptide chain. Preferably, the Fv polypeptide further comprises a polypeptide linker between the V<sub>H</sub> and V<sub>L</sub> domains which enables the sFv to form the desired 20 structure for antigen binding. For a review of sFv, see Pluckthun in The Pharmacology of Monoclonal Antibodies, vol. 113, Rosenberg and Moore eds., Springer-Verlag, New York, pp. 269-315 (1994).

The term "diabodies" refers to small antibody fragments with two antigen-binding sites, which fragments comprise a heavy-chain variable domain (V<sub>H</sub>) connected to a light-chain variable domain (V<sub>L</sub>) in the same polypeptide chain (V<sub>H</sub>-V<sub>L</sub>). By using a linker that is too short to allow pairing between the two 25 domains on the same chain, the domains are forced to pair with the complementary domains of another chain and create two antigen-binding sites. Diabodies are described more fully in, for example, EP 404,097; WO 93/11161; and Hollinger et al., Proc. Natl. Acad. Sci. USA, 90:6444-6448 (1993).

An "isolated" antibody is one which has been identified and separated and/or recovered from a component of its natural environment. Contaminant components of its natural environment are materials 30 which would interfere with diagnostic or therapeutic uses for the antibody, and may include enzymes, hormones, and other proteinaceous or nonproteinaceous solutes. In preferred embodiments, the antibody will be purified (1) to greater than 95% by weight of antibody as determined by the Lowry method, and most preferably more than 99% by weight, (2) to a degree sufficient to obtain at least 15 residues of N-terminal or internal amino acid sequence by use of a spinning cup sequenator, or (3) to homogeneity by SDS-PAGE 35 under reducing or nonreducing conditions using Coomassie blue or, preferably, silver stain. Isolated antibody includes the antibody in situ within recombinant cells since at least one component of the antibody's natural environment will not be present. Ordinarily, however, isolated antibody will be prepared by at least one purification step.

An antibody that "specifically binds to" or is "specific for" a particular polypeptide or an epitope on a particular polypeptide is one that binds to that particular polypeptide or epitope on a particular polypeptide without substantially binding to any other polypeptide or polypeptide epitope.

5 The word "label" when used herein refers to a detectable compound or composition which is conjugated directly or indirectly to the antibody so as to generate a "labeled" antibody. The label may be detectable by itself (e.g. radioisotope labels or fluorescent labels) or, in the case of an enzymatic label, may catalyze chemical alteration of a substrate compound or composition which is detectable.

By "solid phase" is meant a non-aqueous matrix to which the antibody of the present invention can adhere. Examples of solid phases encompassed herein include those formed partially or entirely of glass (e.g., controlled pore glass), polysaccharides (e.g., agarose), polyacrylamides, polystyrene, polyvinyl alcohol and silicones. In certain embodiments, depending on the context, the solid phase can comprise the well of an assay plate; in others it is a purification column (e.g., an affinity chromatography column). This term also includes a discontinuous solid phase of discrete particles, such as those described in U.S. Patent No. 4,275,149.

15 A "liposome" is a small vesicle composed of various types of lipids, phospholipids and/or surfactant which is useful for delivery of a drug (such as a PRO polypeptide or antibody thereto) to a mammal. The components of the liposome are commonly arranged in a bilayer formation, similar to the lipid arrangement of biological membranes.

A "small molecule" is defined herein to have a molecular weight below about 500 Daltons.

20 The term "immune related disease" means a disease in which a component of the immune system of a mammal causes, mediates or otherwise contributes to a morbidity in the mammal. Also included are diseases in which stimulation or intervention of the immune response has an ameliorative effect on progression of the disease. Included within this term are immune-mediated inflammatory diseases, non-immune-mediated inflammatory diseases, infectious diseases, immunodeficiency diseases, neoplasia, etc.

25 The term "T cell mediated disease" means a disease in which T cells directly or indirectly mediate or otherwise contribute to a morbidity in a mammal. The T cell mediated disease may be associated with cell mediated effects, lymphokine mediated effects, etc., and even effects associated with B cells if the B cells are stimulated, for example, by the lymphokines secreted by T cells.

30 Examples of immune-related and inflammatory diseases, some of which are immune or T cell mediated, which can be treated according to the invention include systemic lupus erythematosis, rheumatoid arthritis, juvenile chronic arthritis, spondyloarthropathies, systemic sclerosis (scleroderma), idiopathic inflammatory myopathies (dermatomyositis, polymyositis), Sjögren's syndrome, systemic vasculitis, sarcoidosis, autoimmune hemolytic anemia (immune pancytopenia, paroxysmal nocturnal hemoglobinuria), autoimmune thrombocytopenia (idiopathic thrombocytopenic purpura, immune-mediated thrombocytopenia), 35 thyroiditis (Grave's disease, Hashimoto's thyroiditis, juvenile lymphocytic thyroiditis, atrophic thyroiditis); diabetes mellitus, immune-mediated renal disease (glomerulonephritis, tubulointerstitial nephritis), demyelinating diseases of the central and peripheral nervous systems such as multiple sclerosis, idiopathic demyelinating polyneuropathy or Guillain-Barré syndrome, and chronic inflammatory demyelinating polyneuropathy, hepatobiliary diseases such as infectious hepatitis (hepatitis A, B, C, D, E 40 and other non-hepatotropic viruses), autoimmune chronic active hepatitis, primary biliary cirrhosis,

granulomatous hepatitis, and sclerosing cholangitis, inflammatory bowel disease (ulcerative colitis: Crohn's disease), gluten-sensitive enteropathy, and Whipple's disease, autoimmune or immune-mediated skin diseases including bullous skin diseases, erythema multiforme and contact dermatitis, psoriasis, allergic diseases such as asthma, allergic rhinitis, atopic dermatitis, food hypersensitivity and urticaria, immunologic diseases of the lung such as eosinophilic pneumonias, idiopathic pulmonary fibrosis and hypersensitivity pneumonitis, transplantation associated diseases including graft rejection and graft -versus-host-disease. Infectious diseases including viral diseases such as AIDS (HIV infection), hepatitis A, B, C, D, and E, herpes, etc., bacterial infections, fungal infections, protozoal infections and parasitic infections.

The term "effective amount" is a concentration or amount of a PRO polypeptide and/or agonist/antagonist which results in achieving a particular stated purpose. An "effective amount" of a PRO polypeptide or agonist or antagonist thereof may be determined empirically. Furthermore, a "therapeutically effective amount" is a concentration or amount of a PRO polypeptide and/or agonist/antagonist which is effective for achieving a stated therapeutic effect. This amount may also be determined empirically.

The term "cytotoxic agent" as used herein refers to a substance that inhibits or prevents the function of cells and/or causes destruction of cells. The term is intended to include radioactive isotopes (e.g., I<sup>131</sup>, I<sup>125</sup>, Y<sup>90</sup> and Re<sup>186</sup>), chemotherapeutic agents, and toxins such as enzymatically active toxins of bacterial, fungal, plant or animal origin, or fragments thereof.

A "chemotherapeutic agent" is a chemical compound useful in the treatment of cancer. Examples of chemotherapeutic agents include adriamycin, doxorubicin, epirubicin, 5-fluorouracil, cytosine arabinoside ("Ara-C"), cyclophosphamide, thiotepa, busulfan, cytoxin, taxoids, e.g., paclitaxel (Taxol, Bristol-Myers Squibb Oncology, Princeton, NJ), and doxetaxel (Taxotere, Rhône-Poulenc Rorer, Antony, France), toxotere, methotrexate, cisplatin, melphalan, vinblastine, bleomycin, etoposide, ifosfamide, mitomycin C, mitoxantrone, vincristine, vinorelbine, carboplatin, teniposide, daunomycin, carminomycin, aminopterin, dactinomycin, mitomycins, esperamicins (see U.S. Pat. No. 4,675,187), melphalan and other related nitrogen mustards. Also included in this definition are hormonal agents that act to regulate or inhibit hormone action on tumors such as tamoxifen and onapristone.

A "growth inhibitory agent" when used herein refers to a compound or composition which inhibits growth of a cell, especially cancer cell overexpressing any of the genes identified herein, either *in vitro* or *in vivo*. Thus, the growth inhibitory agent is one which significantly reduces the percentage of cells overexpressing such genes in S phase. Examples of growth inhibitory agents include agents that block cell cycle progression (at a place other than S phase), such as agents that induce G1 arrest and M-phase arrest. Classical M-phase blockers include the vincas (vincristine and vinblastine), taxol, and topo II inhibitors such as doxorubicin, epirubicin, daunorubicin, etoposide, and bleomycin. Those agents that arrest G1 also spill over into S-phase arrest, for example, DNA alkylating agents such as tamoxifen, prednisone, dacarbazine, mechlorethamine, cisplatin, methotrexate, 5-fluorouracil, and ara-C. Further information can be found in *The Molecular Basis of Cancer*, Mendelsohn and Israel, eds., Chapter 1, entitled "Cell cycle regulation, oncogens, and antineoplastic drugs" by Murakami *et al.* (WB Saunders: Philadelphia, 1995), especially p. 13.

The term "cytokine" is a generic term for proteins released by one cell population which act on another cell as intercellular mediators. Examples of such cytokines are lymphokines, monokines, and

traditional polypeptide hormones. Included among the cytokines are growth hormone such as human growth hormone, N-methionyl human growth hormone, and bovine growth hormone; parathyroid hormone; thyroxine; insulin; proinsulin; relaxin; prorelaxin; glycoprotein hormones such as follicle stimulating hormone (FSH), thyroid stimulating hormone (TSH), and luteinizing hormone (LH); hepatic growth factor; 5 fibroblast growth factor; prolactin; placental lactogen; tumor necrosis factor- $\alpha$  and - $\beta$ ; mullerian-inhibiting substance; mouse gonadotropin-associated peptide; inhibin; activin; vascular endothelial growth factor; integrin; thrombopoietin (TPO); nerve growth factors such as NGF- $\beta$ ; platelet-growth factor; transforming growth factors (TGFs) such as TGF- $\alpha$  and TGF- $\beta$ ; insulin-like growth factor-I and -II; erythropoietin (EPO); 10 osteoinductive factors; interferons such as interferon- $\alpha$ , - $\beta$ , and - $\gamma$ ; colony stimulating factors (CSFs) such as macrophage-CSF (M-CSF); granulocyte-macrophage-CSF (GM-CSF); and granulocyte-CSF (G-CSF); interleukins (ILs) such as IL-1, IL-1 $\alpha$ , IL-2, IL-3, IL-4, IL-5, IL-6, IL-7, IL-8, IL-9, IL-11, IL-12; a tumor necrosis factor such as TNF- $\alpha$  or TNF- $\beta$ ; and other polypeptide factors including LIF and kit ligand (KL). As used herein, the term cytokine includes proteins from natural sources or from recombinant cell culture and biologically active equivalents of the native sequence cytokines.

15 As used herein, the term "immunoadhesin" designates antibody-like molecules which combine the binding specificity of a heterologous protein (an "adhesin") with the effector functions of immunoglobulin constant domains. Structurally, the immunoadhesins comprise a fusion of an amino acid sequence with the desired binding specificity which is other than the antigen recognition and binding site of an antibody (*i.e.*, is "heterologous"), and an immunoglobulin constant domain sequence. The adhesin part of an immunoadhesin molecule typically is a contiguous amino acid sequence comprising at least the binding site of a receptor or a ligand. The immunoglobulin constant domain sequence in the immunoadhesin may be obtained from any immunoglobulin, such as IgG-1, IgG-2, IgG-3, or IgG-4 subtypes, IgA (including IgA-1 and IgA-2), IgE, 20 IgD or IgM.

25 As used herein, the term "inflammatory cells" designates cells that enhance the inflammatory response such as mononuclear cells, eosinophils, macrophages, and polymorphonuclear neutrophils (PMN).

**Table 1**

45

50

55

**Table 1 (cont<sup>2</sup>)**

```

/*
 */
#include <stdio.h>
5 #include <ctype.h>

#define MAXJMP 16 /* max jumps in a diag */
#define MAXGAP 24 /* don't continue to penalize gaps larger than this */
#define J MPS 1024 /* max jmps in an path */
10 #define MX 4 /* save if there's at least MX-1 bases since last jmp */

#define DMAT 3 /* value of matching bases */
#define DMIS 0 /* penalty for mismatched bases */
#define DINSO 8 /* penalty for a gap */
15 #define DIN S1 1 /* penalty per base */
#define PINS0 8 /* penalty for a gap */
#define PINS1 4 /* penalty per residue */

20 struct jmp {
    short n[MAXJMP]; /* size of jmp (neg for delay) */
    unsigned short x[MAXJMP]; /* base no. of jmp in seq x */
    /* limits seq to 2^16 -1 */
};

25 struct diag {
    int score; /* score at last jmp */
    long offset; /* offset of prev block */
    short ijmp; /* current jmp index */
    struct jmp jp; /* list of jmps */
};

30 struct path {
    int spc; /* number of leading spaces */
    short n[J MPS]; /* size of jmp (gap) */
    int x[J MPS]; /* loc of jmp (last elem before gap) */
};

35 char *ofile; /* output file name */
char *namex[2]; /* seq names: getseqs() */
char *prog; /* prog name for err msgs */
40 char *seqx[2]; /* seqs: getseqs() */
int dmax; /* best diag: nw() */
int dmax0; /* final diag */
int dna; /* set if dna: main() */
45 int endgaps; /* set if penalizing end gaps */
int gapx, gapy; /* total gaps in seqs */
int len0, len1; /* seq lens */
int ngapx, ngapy; /* total size of gaps */
int smax; /* max score: nw() */
int *xbm; /* bitmap for matching */
50 long offset; /* current offset in jmp file */
struct diag *dx; /* holds diagonals */
struct path pp[2]; /* holds path for seqs */

55 char *calloc(), *malloc(), *index(), *strcpy();
char *getseq(), *g_calloc();

```

**Table 1 (cont')**

```

/* Needleman-Wunsch alignment program
*
* usage: progs file1 file2
5   * where file1 and file2 are two dna or two protein sequences.
*   The sequences can be in upper- or lower-case an may contain ambiguity
*   Any lines beginning with ';' '>' or '<' are ignored
*   Max file length is 65535 (limited by unsigned short x in the jmp struct)
*   A sequence with 1/3 or more of its elements ACGTU is assumed to be DNA
10  * Output is in the file "align.out"
*
* The program may create a tmp file in /tmp to hold info about traceback.
* Original version developed under BSD 4.3 on a vax 8650
*/
15 #include "nw.h"
#include "day.h"

static _dbval[26] = {
20   1,14,2,13,0,0,4,11,0,0,12,0,3,15,0,0,0,5,6,8,8,7,9,0,10,0
};

static _pbval[26] = {
25   1, 2|(1<<('D'-'A'))|(1<<('N'-'A')), 4, 8, 16, 32, 64,
   128, 256, 0xFFFFFFFF, 1<<10, 1<<11, 1<<12, 1<<13, 1<<14,
   1<<15, 1<<16, 1<<17, 1<<18, 1<<19, 1<<20, 1<<21, 1<<22,
   1<<23, 1<<24, 1<<25|(1<<('E'-'A'))|(1<<('Q'-'A'))
};

main(ac, av)
30  main
    int      ac;
    char    *av[ ];
{
    prog = av[0];
35  if (ac != 3) {
        sprintf(stderr, "usage: %s file1 file2\n", prog);
        sprintf(stderr, "where file1 and file2 are two dna or two protein sequences.\n");
        sprintf(stderr, "The sequences can be in upper- or lower-case\n");
        sprintf(stderr, "Any lines beginning with ';' or '<' are ignored\n");
        sprintf(stderr, "Output is in the file \"align.out\"\n");
        exit(1);
    }
    namex[0] = av[1];
    namex[1] = av[2];
45  seqx[0] = getseq(namex[0], &len0);
    seqx[1] = getseq(namex[1], &len1);
    xbm = (dna)? _dbval : _pbval;

    endgaps = 0;           /* 1 to penalize endgaps */
50  ofile = "align.out";    /* output file */

    nw();                  /* fill in the matrix, get the possible jmps */
    readjmps();            /* get the actual jmps */
    print();                /* print stats, alignment */
55  cleanup(0);            /* unlink any tmp files */
}

```

**Table 1 (cont')**

```

/* do the alignment, return best score: main()
 * dna: values in Fitch and Smith, PNAS, 80, 1382-1386, 1983
 * pro: PAM 250 values
5   * When scores are equal, we prefer mismatches to any gap, prefer
   * a new gap to extending an ongoing gap, and prefer a gap in seqx
   * to a gap in seq y.
   */
nw()

10  nw
{
    char      *px, *py;          /* seqs and ptrs */
    int       *ndely, *dely;     /* keep track of dely */
    int       ndelx, delx;      /* keep track of delx */
15   int       *tmp;           /* for swapping row0, row1 */
    int       mis;             /* score for each type */
    int       ins0, ins1;       /* insertion penalties */
    register  id;              /* diagonal index */
    register  ij;              /* jmp index */
20   register  *col0, *col1;   /* score for curr, last row */
    register  xx, yy;          /* index into seqs */

    dx = (struct diag *)g_calloc("to get diags", len0+len1+1, sizeof(struct diag));

25   ndely = (int *)g_calloc("to get ndely", len1+1, sizeof(int));
    dely = (int *)g_calloc("to get dely", len1+1, sizeof(int));
    col0 = (int *)g_calloc("to get col0", len1+1, sizeof(int));
    col1 = (int *)g_calloc("to get col1", len1+1, sizeof(int));
    ins0 = (dna)? DINS0 : PINS0;
30   ins1 = (dna)? DINS1 : PINS1;

    smax = -10000;
    if (endgaps) {
        for (col0[0] = dely[0] = -ins0, yy = 1; yy <= len1; yy++) {
            col0[yy] = dely[yy] = col0[yy-1] - ins1;
            ndely[yy] = yy;
        }
        col0[0] = 0;          /* Waterman Bull Math Biol 84 */
        }
40   else
        for (yy = 1; yy <= len1; yy++)
            dely[yy] = -ins0;

45   /* fill in match matrix
    */
    for (px = seqx[0], xx = 1; xx <= len0; px++, xx++) {
        /* initialize first entry in col
        */
        if (endgaps) {
            if (xx == 1)
                col1[0] = delx = -(ins0+ins1);
            else
                col1[0] = delx = col0[0] - ins1;
            ndelx = xx;
        }
55   else {
            col1[0] = 0;
            delx = -ins0;
            ndelx = 0;
        }
60   }
}

```

**Table 1 (cont?)**

...nw

```

for (py = seqx[1], yy = 1; yy <= len1; py++, yy++) {
    mis = col0[yy-1];
    if (dna)
        mis += (xbm[*px-'A']&xbm[*py-'A'])? DMAT : DMIS;
    else
        mis += _day[*px-'A'][*py-'A'];

    /* update penalty for del in x seq;
     * favor new del over ongoing del
     * ignore MAXGAP if weighting endgaps
     */
    if (endgaps || ndely[yy] < MAXGAP) {
        if (col0[yy] - ins0 >= dely[yy]) {
            dely[yy] = col0[yy] - (ins0+ins1);
            ndely[yy] = 1;
        } else {
            dely[yy] -= ins1;
            ndely[yy]++;
        }
    } else {
        if (col0[yy] - (ins0+ins1) >= dely[yy]) {
            dely[yy] = col0[yy] - (ins0+ins1);
            ndely[yy] = 1;
        } else
            ndely[yy]++;
    }

    /* update penalty for del in y seq;
     * favor new del over ongoing del
     */
    if (endgaps || ndelx < MAXGAP) {
        if (col1[yy-1] - ins0 >= delx) {
            delx = col1[yy-1] - (ins0+ins1);
            ndelx = 1;
        } else {
            delx -= ins1;
            ndelx++;
        }
    } else {
        if (col1[yy-1] - (ins0+ins1) >= delx) {
            delx = col1[yy-1] - (ins0+ins1);
            ndelx = 1;
        } else
            ndelx++;
    }

    /* pick the maximum score; we're favoring
     * mis over any del and delx over dely
     */
}

55

60

```

Table 1 (cont')

...nw

```

id = xx - yy + len1 - 1;
if (mis >= delx && mis >= dely[yy])
5      col1[yy] = mis;
else if (delx >= dely[yy]) {
      col1[yy] = delx;
      ij = dx[id].ijmp;
      if (dx[id].jp.n[0] && (!dna || (ndelx >= MAXJMP
&& xx > dx[id].jp.x[ij]+MX) || mis > dx[id].score+DINS0)) {
10         dx[id].ijmp++;
         if (++ij >= MAXJMP) {
            writejmps(id);
            ij = dx[id].ijmp = 0;
            dx[id].offset = offset;
            offset += sizeof(struct jmp) + sizeof(offset);
15         }
      }
      dx[id].jp.n[ij] = ndelx;
      dx[id].jp.x[ij] = xx;
      dx[id].score = delx;
20   }
else {
      col1[yy] = dely[yy];
      ij = dx[id].ijmp;
25   if (dx[id].jp.n[0] && (!dna || (ndely[yy] >= MAXJMP
&& xx > dx[id].jp.x[ij]+MX) || mis > dx[id].score+DINS0)) {
            dx[id].ijmp++;
            if (++ij >= MAXJMP) {
30               writejmps(id);
               ij = dx[id].ijmp = 0;
               dx[id].offset = offset;
               offset += sizeof(struct jmp) + sizeof(offset);
            }
      }
      dx[id].jp.n[ij] = -ndely[yy];
      dx[id].jp.x[ij] = xx;
      dx[id].score = dely[yy];
35   }
if (xx == len0 && yy < len1) {
40     /* last col
        */
        if (endgaps)
          col1[yy] -= ins0+ins1*(len1-yy);
45     if (col1[yy] > smax) {
          smax = col1[yy];
          dmax = id;
        }
50   }
if (endgaps && xx < len0)
55   col1[yy-1] -= ins0+ins1*(len0-xx);
if (col1[yy-1] > smax) {
      smax = col1[yy-1];
      dmax = id;
    }
tmp = col0; col0 = col1; col1 = tmp;
60   }
(void) free((char *)ndely);
(void) free((char *)dely);
(void) free((char *)col0);
(void) free((char *)col1);
}

```

Table 1 (cont')

```

/*
*
* print() -- only routine visible outside this module
5
* static:
* getmat() -- trace back best path, count matches: print()
* pr_align() -- print alignment of described in array p[ ]; print()
* dumpblock() -- dump a block of lines with numbers, stars: pr_align()
10
* nums() -- put out a number line: dumpblock()
* putline() -- put out a line (name, [num], seq, [num]): dumpblock()
* stars() - -put a line of stars: dumpblock()
* stripname() -- strip any path and prefix from a seqname
*/
15
#include "nw.h"

#define SPC      3
#define P_LINE   256    /* maximum output line */
20 #define P_SPC   3    /* space between name or num and seq */

extern _day[26][26];
int olen;           /* set output line length */
FILE *fx;           /* output file */
25

print()
{
    int lx, ly, firstgap, lastgap; /* overlap */

30    if ((fx = fopen(ofile, "w")) == 0) {
        fprintf(stderr, "%s: can't write %s\n", prog, ofile);
        cleanup(1);
    }
35    sprintf(fx, "<first sequence: %s (length = %d)\n", namex[0], len0);
    sprintf(fx, "<second sequence: %s (length = %d)\n", namex[1], len1);
    olen = 60;
    lx = len0;
    ly = len1;
40    firstgap = lastgap = 0;
    if (dmax < len1 - 1) { /* leading gap in x */
        pp[0].spc = firstgap = len1 - dmax - 1;
        ly -= pp[0].spc;
    }
45    else if (dmax > len1 - 1) { /* leading gap in y */
        pp[1].spc = firstgap = dmax - (len1 - 1);
        lx -= pp[1].spc;
    }
50    if (dmax0 < len0 - 1) { /* trailing gap in x */
        lastgap = len0 - dmax0 - 1;
        lx -= lastgap;
    }
55    else if (dmax0 > len0 - 1) { /* trailing gap in y */
        lastgap = dmax0 - (len0 - 1);
        ly -= lastgap;
    }
    getmat(lx, ly, firstgap, lastgap);
    pr_align();
}
60

```

Table 1 (cont')

```

/*
 * trace back the best path, count matches
 */
5 static
getmat(lx, ly, firstgap, lastgap) getmat
{
    int      lx, ly;          /* "core" (minus endgaps) */
    int      firstgap, lastgap; /* leading/trailing overlap */
10   {
        int      nm, i0, i1, siz0, siz1;
        char     outx[32];
        double   pct;
        register int n0, n1;
        register char *p0, *p1;
15   /*
     * get total matches, score
     */
        i0 = i1 = siz0 = siz1 = 0;
        p0 = seqx[0] + pp[1].spc;
20   p1 = seqx[1] + pp[0].spc;
        n0 = pp[1].spc + 1;
        n1 = pp[0].spc + 1;

        nm = 0;
25   while (*p0 && *p1) {
            if (siz0) {
                p1++;
                n1++;
                siz0--;
30           }
            else if (siz1) {
                p0++;
                n0++;
                siz1--;
35           }
            else {
                if (xbm[*p0-'A']&xbm[*p1-'A'])
                    nm++;
40           if (n0++ == pp[0].x[i0])
                    siz0 = pp[0].n[i0++];
                if (n1++ == pp[1].x[i1])
                    siz1 = pp[1].n[i1++];
                p0++;
                p1++;
45           }
            }
        }

/* pct homology:
 * if penalizing endgaps, base is the shorter seq
50   * else, knock off overhangs and take shorter core
 */
        if (endgaps)
            lx = (len0 < len1)? len0 : len1;
        else
55   lx = (lx < ly)? lx : ly;
        pct = 100.*(double)nm/(double)lx;
        fprintf(fx, "\n");
        fprintf(fx, "<%d match%s in an overlap of %d: %.2f percent similarity\n",
60   nm, (nm == 1)? ":" : "es", lx, pct);

```

**Table 1 (cont')**

```

5      sprintf(fx, "<gaps in first sequence: %d", gapx);           ...getmat
if (gapx) {
    (void) sprintf(outx, " (%d %s%s)", ngapx, (DNA)? "base": "residue", (ngapx == 1)? "": "s");
    sprintf(fx, "%s", outx);

10     sprintf(fx, ", gaps in second sequence: %d", gapy);
if (gapy) {
    (void) sprintf(outx, " (%d %s%s)", ngapy, (DNA)? "base": "residue", (ngapy == 1)? "": "s");
    sprintf(fx, "%s", outx);
}

15     if (DNA)
        sprintf(fx,
        "<score: %d (match = %d, mismatch = %d, gap penalty = %d + %d per base)\n",
        smax, DMAT, DMIS, DINS0, DINS1);
else
20       sprintf(fx,
        "<score: %d (Dayhoff PAM 250 matrix, gap penalty = %d + %d per residue)\n",
        smax, PINS0, PINS1);
if (endgaps)
25       sprintf(fx,
        "<endgaps penalized. left endgap: %d %s%s, right endgap: %d %s%s\n",
        firstgap, (DNA)? "base": "residue", (firstgap == 1)? "": "s",
        lastgap, (DNA)? "base": "residue", (lastgap == 1)? "": "s");
else
30       sprintf(fx, "<endgaps not penalized\n");

35     static nm;          /* matches in core -- for checking */
static lmax;         /* lengths of stripped file names */
static ij[2];         /* jmp index for a path */
static nc[2];         /* number at start of current line */
static ni[2];         /* current elem number -- for gapping */
static siz[2];
static char *ps[2];    /* ptr to current element */
static char *po[2];    /* ptr to next output char slot */
40     static char out[2][P_LINE]; /* output line */
static char star[P_LINE]; /* set by stars() */

/*
 * print alignment of described in struct path pp[]
 */
45     static
pr_align()
{
    int nn;          /* char count */
    int more;
50     register i;

    for (i = 0, lmax = 0; i < 2; i++) {
        nn = stripname(namex[i]);
        if (nn > lmax)
            lmax = nn;

        nc[i] = 1;
        ni[i] = 1;
        siz[i] = ij[i] = 0;
        ps[i] = seqx[i];
        po[i] = out[i];
    }
}

```

Table 1 (cont')

```

for (nn = nm = 0, more = 1; more; ) {
    for (i = more = 0; i < 2; i++) {
        /*
         * do we have more of this sequence?
         */
        if (!*ps[i])
            continue;
    10   more++;

    if (pp[i].spc) { /* leading space */
        *po[i]++ = ' ';
        pp[i].spc--;
    15   }
    else if (siz[i]) { /* in a gap */
        *po[i]++ = ' ';
        siz[i]--;
    20   }
    else { /* we're putting a seq element
        */
        *po[i] = *ps[i];
        if (islower(*ps[i]))
            *ps[i] = toupper(*ps[i]);
        po[i]++;
        ps[i]++;
        /*
         * are we at next gap for this seq?
         */
        if (ni[i] == pp[i].x[ij[i]]) {
            /*
             * we need to merge all gaps
             * at this location
             */
            siz[i] = pp[i].n[ij[i]++];
            while (ni[i] == pp[i].x[ij[i]])
                siz[i] += pp[i].n[ij[i]++];
        40           }
        ni[i]++;
    }
    45   }
    if (++nn == olen || !more && nn) {
        dumpblock();
        for (i = 0; i < 2; i++)
            po[i] = out[i];
        nn = 0;
    }
50   }

/*
 * dump a block of lines, including numbers, stars: pr_align()
 */
static
dumpblock()
{
    register i;
    for (i = 0; i < 2; i++)
        *po[i]-- = '0';
}

```

**Table 1 (cont')**

```

...dumpblock

5   (void) putc('\n', fx);
    for (i = 0; i < 2; i++) {
        if (*out[i] && (*out[i] != ' ' || *(po[i]) != ' '))
            if (i == 0)
                nums(i);
            if (i == 0 && *out[1])
                stars();
            putline(i);
        if (i == 0 && *out[1])
            fprintf(fx, star);
        if (i == 1)
            nums(i);
    }
}

20  /*
 * put out a number line: dumpblock()
 */
static
nums(ix)
25  int      ix;      /* index in out[ ] holding seq line */
{
    char      nline[P_LINE];
    register  i, j;
    register char *pn, *px, *py;

30  for (pn = nline, i = 0; i < lmax+P_SPC; i++, pn++)
    *pn = ' ';
    for (i = nc[ix], py = out[ix]; *py; py++, pn++) {
        if (*py == ' ' || *py == '-')
            *pn = '-';
        else {
            if (i%10 == 0 || (i == 1 && nc[ix] != 1)) {
                j = (i < 0)? -i : i;
                for (px = pn; j; j /= 10, px--)
                    *px = j%10 + '0';
                if (i < 0)
                    *px = '-';
            }
            else
                *pn = '-';
            i++;
        }
    }
    *pn = '\0';
    nc[ix] = i;
    for (pn = nline; *pn; pn++)
        (void) putc(*pn, fx);
    (void) putc('\n', fx);
}

55  /*
 * put out a line (name, [num], seq, [num]): dumpblock()
 */
static
putline(ix)
60  putline(ix)
    int      ix;
}

```

**nums**

**putline**

Table 1 (cont')

...putline

```

5      int          i;
register char    *px;

for (px = namex[ix], i = 0; *px && *px != ':'; px++, i++)
    (void) putc(*px, fx);
for (; i < lmax+P_SPC; i++)
    (void) putc(' ', fx);

10     /* these count from 1:
        * ni[ ] is current element (from 1)
        * nc[ ] is number at start of current line
        */
15     for (px = out[ix]; *px; px++)
    (void) putc(*px&0x7F, fx);
    (void) putc('\n', fx);
}

20     /*

25     * put a line of stars (seqs always in out[0], out[1]): dumpblock()
     */
25 static
stars()

30     stars
{
    int          i;
register char    *p0, *p1, cx, *px;

if (!*out[0] || (*out[0] == ' ' && *(po[0]) == ') ||
    !*out[1] || (*out[1] == ' ' && *(po[1]) == ') )
    return;
35     px = star;
for (i = lmax+P_SPC; i; i--)
    *px++ = ' ';

40     for (p0 = out[0], p1 = out[1]; *p0 && *p1; p0++, p1++) {
        if (isalpha(*p0) && isalpha(*p1)) {

45         if (xbm[*p0-'A']&xbm[*p1-'A']) {
            cx = '*';
            nm++;
        }
        else if (!dna && _day[*p0-'A'][*p1-'A'] > 0)
            cx = ':';
        else
            cx = ' ';
50         }
        else
            cx = ' ';
        *px++ = cx;
    }
55     *px++ = '\n';
    *px = '\0';
}
}

```

Table 1 (cont')

```
/*
 * strip path or prefix from pn, return len: pr_align()
 */
5 static
stripname(pn)
stripname
char *pn; /* file name (may be path) */

10 {
register char *px, *py;

py = 0;
for (px = pn; *px; px++)
if (*px == '/')
15     py = px + 1;
if (py)
(void) strcpy(pn, py);
return(strlen(pn));
20 }
```

25

30

35

40

45

50

55

60

Table 1 (cont')

```

/*
 * cleanup() -- cleanup any tmp file
 * getseq() -- read in seq, set dna, len, maxlen
5  * g_calloc() -- calloc() with error checkin
 * readjmps() -- get the good jmps, from tmp file if necessary
 * writejmps() -- write a filled array of jmps to a tmp file: nw()
 */
10 #include "nw.h"
#include <sys/file.h>

char *jname = "/tmp/homgXXXXXX";           /* tmp file for jmps */
FILE *fj;

15 int cleanup();                           /* cleanup tmp file */
long lseek();

/*
 * remove any tmp file if we blow
20 */
cleanup(i)
{
    int i;
    if (fj)
        (void) unlink(jname);
    exit(i);
}

/*
30 * read, return ptr to seq, set dna, len, maxlen
 * skip lines starting with ';', '<', or '>'
 * seq in upper or lower case
 */
char *
35 getseq(file, len)                      cleanup
{
    char *file;   /* file name */
    int *len;    /* seq len */
    {
        char line[1024], *pseq;
40    register char *px, *py;
        int natgc, tlen;
        FILE *fp;
    }

    if ((fp = fopen(file, "r")) == 0) {
45        fprintf(stderr, "%s: can't read %s\n", prog, file);
        exit(1);
    }
    tlen = natgc = 0;
    while (fgets(line, 1024, fp)) {
50        if (*line == ';' || *line == '<' || *line == '>')
            continue;
        for (px = line; *px != '\n'; px++)
            if (isupper(*px) || islower(*px))
                tlen++;
    }
55    if ((pseq = malloc((unsigned)(tlen+6))) == 0)
        fprintf(stderr, "%s: malloc() failed to get %d bytes for %s\n", prog, tlen+6, file);
        exit(1);
    }
60    pseq[0] = pseq[1] = pseq[2] = pseq[3] = '\0';

```

Table 1 (cont')

...getseq

```

5      py = pseq + 4;
     *len = tlen;
     rewind(fp);

10     while (fgets(line, 1024, fp)) {
           if (*line == ';' || *line == '<' || *line == '>')
               continue;
           for (px = line; *px != '\n'; px++) {
               if (isupper(*px))
                   *py++ = *px;
               else if (islower(*px))
                   *py++ = toupper(*px);
15           if (index("ATGCU", *(py-1)))
               natgc++;
           }
           *py++ = '\0';
20           *py = '\0';
           (void) fclose(fp);
           dna = natgc > (tlen/3);
           return(pseq+4);
       }

25     char   *
g_calloc(msg, nx, sz)
30     {
           char   *msg;          /* program, calling routine */
           int    nx, sz;         /* number and size of elements */
           char   *px, *calloc();
           if ((px = calloc((unsigned)nx, (unsigned)sz)) == 0) {
               if (*msg) {
35                   fprintf(stderr, "%s: g_calloc() failed %s (n=%d, sz=%d)\n", prog, msg, nx, sz);
                   exit(1);
               }
           }
           return(px);
       }

40     /*
45     * get final jmps from dx[ ] or tmp file, set pp[ ], reset dmax: main()
46     */
readjmps()
47     readjmps()
48     {
50     int        fd = -1;
     int        siz, i0, i1;
     register  i, j, xx;

55     if (fj) {
           (void) fclose(fj);
           if ((fd = open(jname, O_RDONLY, 0)) < 0) {
               fprintf(stderr, "%s: can't open() %s\n", prog, jname);
               cleanup(1);
           }
       }
60     for (i = i0 = i1 = 0, dmax0 = dmax, xx = len0; ; i++) {
           while (1) {
               for (j = dx[dmax].ijmp; j >= 0 && dx[dmax].jp.x[j] >= xx; j--)
               ;
           }
       }
   }

```

g\_calloc

**Table 1 (cont')****...readjmps**

```

5      if (j < 0 && dx[dmax].offset && fj) {
          (void) lseek(fd, dx[dmax].offset, 0);
          (void) read(fd, (char *)&dx[dmax].jp, sizeof(struct jmp));
          (void) read(fd, (char *)&dx[dmax].offset, sizeof(dx[dmax].offset));
          dx[dmax].ijmp = MAXJMP-1;
      }
10     else
      break;
  }
15     if (i >= JMPS) {
          fprintf(stderr, "%s: too many gaps in alignment\n", prog);
          cleanup(1);
  }
20     if (j >= 0) {
          siz = dx[dmax].jp.n[j];
          xx = dx[dmax].jp.x[j];
          dmax += siz;
          if (siz < 0) { /* gap in second seq */
              pp[1].n[i1] = -siz;
              xx += siz;
              /* id = xx - yy + len1 - 1
               */
              pp[1].x[i1] = xx - dmax + len1 - 1;
              gapy++;
              ngapy -= siz;
          }
25         /* ignore MAXGAP when doing endgaps */
          siz = (-siz < MAXGAP || endgaps)? -siz : MAXGAP;
          i1++;
  }
30         else if (siz > 0) { /* gap in first seq */
              pp[0].n[i0] = siz;
              pp[0].x[i0] = xx;
              gapx++;
              ngapx += siz;
          }
35         /* ignore MAXGAP when doing endgaps */
          siz = (siz < MAXGAP || endgaps)? siz : MAXGAP;
          i0++;
  }
40     }
45     else
      break;
  }
45     /* reverse the order of jmps
     */
50     for (j = 0, i0--; j < i0; j++, i0--) {
          i = pp[0].n[j]; pp[0].n[j] = pp[0].n[i0]; pp[0].n[i0] = i;
          i = pp[0].x[j]; pp[0].x[j] = pp[0].x[i0]; pp[0].x[i0] = i;
  }
55     for (j = 0, i1--; j < i1; j++, i1--) {
          i = pp[1].n[j]; pp[1].n[j] = pp[1].n[i1]; pp[1].n[i1] = i;
          i = pp[1].x[j]; pp[1].x[j] = pp[1].x[i1]; pp[1].x[i1] = i;
  }
      if (fd >= 0)
          (void) close(fd);
      if (fj) {
          (void) unlink(jname);
          fj = 0;
          offset = 0;
  }

```

Table 1 (cont')

```
/*
 * write a filled jmp struct offset of the prev one (if any): nw()
 */
5   writejmps(ix)
    {
10     writejmps
      int      ix;
15     {
20       char    *mktemp();
         if (!fj) {
           if (mktemp(jname) < 0) {
             fprintf(stderr, "%s: can't mktemp() %s\n", prog, jname);
             cleanup(1);
           }
           if ((fj = fopen(jname, "w")) == 0) {
             fprintf(stderr, "%s: can't write %s\n", prog, jname);
             exit(1);
           }
         }
         (void) fwrite((char *)&dx[ix].jp, sizeof(struct jmp), 1, fj);
         (void) fwrite((char *)&dx[ix].offset, sizeof(dx[ix].offset), 1, fj);
       }
     }
```

Table 2

PRO	XXXXXXXXXXXXXXXXXX	(Length = 15 amino acids)
Comparison Protein	XXXXXYYYYYYYYY	(Length = 12 amino acids)

5 % amino acid sequence identity =

(the number of identically matching amino acid residues between the two polypeptide sequences as determined by ALIGN-2) divided by (the total number of amino acid residues of the PRO polypeptide) =  
 5 divided by 15 = 33.3%

Table 3

PRO	XXXXXXXXXXXX	(Length = 10 amino acids)
Comparison Protein	XXXXXYYYYYYYZZY	(Length = 15 amino acids)

% amino acid sequence identity =

(the number of identically matching amino acid residues between the two polypeptide sequences as determined by ALIGN-2) divided by (the total number of amino acid residues of the PRO polypeptide) =  
 5 divided by 10 = 50%

Table 4

PRO-DNA	NNNNNNNNNNNNNN	(Length = 14 nucleotides)
Comparison DNA	NNNNNNLLLLLLLLLL	(Length = 16 nucleotides)

% nucleic acid sequence identity =

(the number of identically matching nucleotides between the two nucleic acid sequences as determined by ALIGN-2) divided by (the total number of nucleotides of the PRO-DNA nucleic acid sequence) =  
 6 divided by 14 = 42.9%

Table 5

PRO-DNA	NNNNNNNNNNNN	(Length = 12 nucleotides)
Comparison DNA	NNNNLLLVV	(Length = 9 nucleotides)

30 % nucleic acid sequence identity =

(the number of identically matching nucleotides between the two nucleic acid sequences as determined by ALIGN-2) divided by (the total number of nucleotides of the PRO-DNA nucleic acid sequence) =  
 4 divided by 12 = 33.3%

~35 II. Compositions and Methods of the Invention

A. Full-Length PRO Polypeptides

The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO polypeptides. In particular, cDNAs encoding various PRO polypeptides have been identified and isolated, as disclosed in further detail in the Examples below. However, for sake of simplicity, in the present specification the protein encoded by the full length

native nucleic acid molecules disclosed herein as well as all further native homologues and variants included in the foregoing definition of PRO, will be referred to as "PRO/number", regardless of their origin or mode of preparation.

As disclosed in the Examples below, various cDNA clones have been disclosed. The predicted amino acid sequence can be determined from the nucleotide sequence using routine skill. For the PRO polypeptides and encoding nucleic acids described herein, Applicants have identified what is believed to be the reading frame best identifiable with the sequence information available at the time.

**B. PRO Polypeptide Variants**

In addition to the full-length native sequence PRO polypeptides described herein, it is contemplated that PRO variants can be prepared. PRO variants can be prepared by introducing appropriate nucleotide changes into the PRO DNA, and/or by synthesis of the desired PRO polypeptide. Those skilled in the art will appreciate that amino acid changes may alter post-translational processes of the PRO, such as changing the number or position of glycosylation sites or altering the membrane anchoring characteristics.

Variations in the native full-length sequence PRO or in various domains of the PRO described herein, can be made, for example, using any of the techniques and guidelines for conservative and non-conservative mutations set forth, for instance, in U.S. Patent No. 5,364,934. Variations may be a substitution, deletion or insertion of one or more codons encoding the PRO that results in a change in the amino acid sequence of the PRO as compared with the native sequence PRO. Optionally, the variation is by substitution of at least one amino acid with any other amino acid in one or more of the domains of the PRO. Guidance in determining which amino acid residue may be inserted, substituted or deleted without adversely affecting the desired activity may be found by comparing the sequence of the PRO with that of homologous known protein molecules and minimizing the number of amino acid sequence changes made in regions of high homology. Amino acid substitutions can be the result of replacing one amino acid with another amino acid having similar structural and/or chemical properties, such as the replacement of a leucine with a serine, i.e., conservative amino acid replacements. Insertions or deletions may optionally be in the range of about 1 to 5 amino acids. The variation allowed may be determined by systematically making insertions, deletions or substitutions of amino acids in the sequence and testing the resulting variants for activity exhibited by the full-length or mature native sequence.

PRO polypeptide fragments are provided herein. Such fragments may be truncated at the N-terminus or C-terminus, or may lack internal residues, for example, when compared with a full length native protein. Certain fragments lack amino acid residues that are not essential for a desired biological activity of the PRO polypeptide.

PRO fragments may be prepared by any of a number of conventional techniques. Desired peptide fragments may be chemically synthesized. An alternative approach involves generating PRO fragments by enzymatic digestion, e.g., by treating the protein with an enzyme known to cleave proteins at sites defined by particular amino acid residues, or by digesting the DNA with suitable restriction enzymes and isolating the desired fragment. Yet another suitable technique involves isolating and amplifying a DNA fragment encoding a desired polypeptide fragment, by polymerase chain reaction (PCR). Oligonucleotides that define the desired termini of the DNA fragment are employed at the 5' and 3' primers in the PCR. Preferably, PRO

polypeptide fragments share at least one biological and/or immunological activity with the native PRO polypeptide disclosed herein.

In particular embodiments, conservative substitutions of interest are shown in Table 6 under the heading of preferred substitutions. If such substitutions result in a change in biological activity, then more substantial changes, denominated exemplary substitutions in Table 6, or as further described below in reference to amino acid classes, are introduced and the products screened.

Table 6

	Original Residue	Exemplary Substitutions	Preferred Substitutions
10	Ala (A)	val; leu; ile	val
	Arg (R)	lys; gln; asn	lys
	Asn (N)	gln; his; lys; arg	gln
	Asp (D)	glu	glu
15	Cys (C)	ser	ser
	Gln (Q)	asn	asn
	Glu (E)	asp	asp
	Gly (G)	pro; ala	ala
	His (H)	asn; gln; lys; arg	arg
20	Ile (I)	leu; val; met; ala; phe; norleucine	leu
	Leu (L)	norleucine; ile; val; met; ala; phe	ile
	Lys (K)	arg; gln; asn	arg
	Met (M)	leu; phe; ile	leu
	Phe (F)	leu; val; ile; ala; tyr	leu
25	Pro (P)	ala	ala
	Ser (S)	thr	thr
	Thr (T)	ser	ser
	Trp (W)	tyr; phe	tyr
	Tyr (Y)	trp; phe; thr; ser	phe
30	Val (V)	ile; leu; met; phe; ala; norleucine	leu

Substantial modifications in function or immunological identity of the PRO polypeptide are accomplished by selecting substitutions that differ significantly in their effect on maintaining (a) the structure of the polypeptide backbone in the area of the substitution, for example, as a sheet or helical conformation, (b) the charge or hydrophobicity of the molecule at the target site, or (c) the bulk of the side chain. Naturally occurring residues are divided into groups based on common side-chain properties:

- (1) hydrophobic: norleucine, met, ala, val, leu, ile;
- (2) neutral hydrophilic: cys, ser, thr;
- (3) acidic: asp, glu;
- 40 (4) basic: asn, gln, his, lys, arg;
- (5) residues that influence chain orientation: gly, pro; and
- (6) aromatic: trp, tyr, phe.

Non-conservative substitutions will entail exchanging a member of one of these classes for another class. Such substituted residues also may be introduced into the conservative substitution sites or, more preferably, into the remaining (non-conserved) sites.

The variations can be made using methods known in the art such as oligonucleotide-mediated (site-directed) mutagenesis, alanine scanning, and PCR mutagenesis. Site-directed mutagenesis [Carter et al., *Nucl. Acids Res.*, 13:4331 (1986); Zoller et al., *Nucl. Acids Res.*, 10:6487 (1987)], cassette mutagenesis

[Wells et al., Gene, 34:315 (1985)], restriction selection mutagenesis [Wells et al., Philos. Trans. R. Soc. London SerA, 317:415 (1986)] or other known techniques can be performed on the cloned DNA to produce the PRO variant DNA.

Scanning amino acid analysis can also be employed to identify one or more amino acids along a contiguous sequence. Among the preferred scanning amino acids are relatively small, neutral amino acids. Such amino acids include alanine, glycine, serine, and cysteine. Alanine is typically a preferred scanning amino acid among this group because it eliminates the side-chain beyond the beta-carbon and is less likely to alter the main-chain conformation of the variant [Cunningham and Wells, Science, 244: 1081-1085 (1989)]. Alanine is also typically preferred because it is the most common amino acid. Further, it is frequently found in both buried and exposed positions [Creighton, The Proteins, (W.H. Freeman & Co., N.Y.); Chothia, J. Mol. Biol., 150:1 (1976)]. If alanine substitution does not yield adequate amounts of variant, an isoteric amino acid can be used.

### C. Modifications of PRO

Covalent modifications of PRO are included within the scope of this invention. One type of covalent modification includes reacting targeted amino acid residues of a PRO polypeptide with an organic derivatizing agent that is capable of reacting with selected side chains or the N- or C-terminal residues of the PRO. Derivatization with bifunctional agents is useful, for instance, for crosslinking PRO to a water-insoluble support matrix or surface for use in the method for purifying anti-PRO antibodies, and vice-versa. Commonly used crosslinking agents include, e.g., 1,1-bis(diazoacetyl)-2-phenylethane, glutaraldehyde, N-hydroxysuccinimide esters, for example, esters with 4-azidosalicylic acid, homobifunctional imidoesters, including disuccinimidyl esters such as 3,3'-dithiobis(succinimidylpropionate), bifunctional maleimides such as bis-N-maleimido-1,8-octane and agents such as methyl-3-[(p-azidophenyl)dithio]propioimidate.

Other modifications include deamidation of glutaminyl and asparaginyl residues to the corresponding glutamyl and aspartyl residues, respectively, hydroxylation of proline and lysine, phosphorylation of hydroxyl groups of seryl or threonyl residues, methylation of the  $\alpha$ -amino groups of lysine, arginine, and histidine side chains [T.E. Creighton, Proteins: Structure and Molecular Properties, W.H. Freeman & Co., San Francisco, pp. 79-86 (1983)], acetylation of the N-terminal amine, and amidation of any C-terminal carboxyl group.

Another type of covalent modification of the PRO polypeptide included within the scope of this invention comprises altering the native glycosylation pattern of the polypeptide. "Altering the native glycosylation pattern" is intended for purposes herein to mean deleting one or more carbohydrate moieties found in native sequence PRO (either by removing the underlying glycosylation site or by deleting the glycosylation by chemical and/or enzymatic means), and/or adding one or more glycosylation sites that are not present in the native sequence PRO. In addition, the phrase includes qualitative changes in the glycosylation of the native proteins, involving a change in the nature and proportions of the various carbohydrate moieties present.

Addition of glycosylation sites to the PRO polypeptide may be accomplished by altering the amino acid sequence. The alteration may be made, for example, by the addition of, or substitution by, one or more serine or threonine residues to the native sequence PRO (for O-linked glycosylation sites). The PRO amino acid sequence may optionally be altered through changes at the DNA level, particularly by mutating the

DNA encoding the PRO polypeptide at preselected bases such that codons are generated that will translate into the desired amino acids.

Another means of increasing the number of carbohydrate moieties on the PRO polypeptide is by chemical or enzymatic coupling of glycosides to the polypeptide. Such methods are described in the art,

5 e.g., in WO 87/05330 published 11 September 1987, and in Aplin and Wriston, CRC Crit. Rev. Biochem., pp. 259-306 (1981).

Removal of carbohydrate moieties present on the PRO polypeptide may be accomplished chemically or enzymatically or by mutational substitution of codons encoding for amino acid residues that serve as targets for glycosylation. Chemical deglycosylation techniques are known in the art and described, 10 for instance, by Hakimuddin, et al., Arch. Biochem. Biophys., 259:52 (1987) and by Edge et al., Anal. Biochem., 118:131 (1981). Enzymatic cleavage of carbohydrate moieties on polypeptides can be achieved by the use of a variety of endo- and exo-glycosidases as described by Thotakura et al., Meth. Enzymol., 138:350 (1987).

Another type of covalent modification of PRO comprises linking the PRO polypeptide to one of a 15 variety of nonproteinaceous polymers, e.g., polyethylene glycol (PEG), polypropylene glycol, or polyoxyalkylenes, in the manner set forth in U.S. Patent Nos. 4,640,835; 4,496,689; 4,301,144; 4,670,417; 4,791,192 or 4,179,337.

The PRO of the present invention may also be modified in a way to form a chimeric molecule comprising PRO fused to another, heterologous polypeptide or amino acid sequence.

20 In one embodiment, such a chimeric molecule comprises a fusion of the PRO with a tag polypeptide which provides an epitope to which an anti-tag antibody can selectively bind. The epitope tag is generally placed at the amino- or carboxyl- terminus of the PRO. The presence of such epitope-tagged forms of the PRO can be detected using an antibody against the tag polypeptide. Also, provision of the epitope tag enables the PRO to be readily purified by affinity purification using an anti-tag antibody or

25 another type of affinity matrix that binds to the epitope tag. Various tag polypeptides and their respective antibodies are well known in the art. Examples include poly-histidine (poly-his) or poly-histidine-glycine (poly-his-gly) tags; the flu HA tag polypeptide and its antibody 12CA5 [Field et al., Mol. Cell. Biol., 8:2159-2165 (1988)]; the c-myc tag and the 8F9, 3C7, 6E10, G4, B7 and 9E10 antibodies thereto [Evan et al., Molecular and Cellular Biology, 5:3610-3616 (1985)]; and the Herpes Simplex virus glycoprotein D (gD)

30 tag and its antibody [Paborsky et al., Protein Engineering, 3(6):547-553 (1990)]. Other tag polypeptides include the Flag-peptide [Hopp et al., BioTechnology, 6:1204-1210 (1988)]; the KT3 epitope peptide [Martin et al., Science, 255:192-194 (1992)]; an alpha-tubulin epitope peptide [Skinner et al., J. Biol. Chem., 266:15163-15166 (1991)]; and the T7 gene 10 protein peptide tag [Lutz-Freyermuth et al., Proc. Natl. Acad. Sci. USA, 87:6393-6397 (1990)].

35 In an alternative embodiment, the chimeric molecule may comprise a fusion of the PRO with an immunoglobulin or a particular region of an immunoglobulin. For a bivalent form of the chimeric molecule (also referred to as an "immunoadhesin"), such a fusion could be to the Fc region of an IgG molecule. The Ig fusions preferably include the substitution of a soluble (transmembrane domain deleted or inactivated) form of a PRO polypeptide in place of at least one variable region within an Ig molecule. In a particularly 40 preferred embodiment, the immunoglobulin fusion includes the hinge, CH2 and CH3, or the hinge, CH1,

CH<sub>2</sub> and CH<sub>3</sub> regions of an IgG1 molecule. For the production of immunoglobulin fusions see also US Patent No. 5,428,130 issued June 27, 1995.

#### D. Preparation of PRO

The description below relates primarily to production of PRO by culturing cells transformed or 5 transfected with a vector containing PRO nucleic acid. It is, of course, contemplated that alternative methods, which are well known in the art, may be employed to prepare PRO. For instance, the PRO sequence, or portions thereof, may be produced by direct peptide synthesis using solid-phase techniques [see, e.g., Stewart et al., Solid-Phase Peptide Synthesis, W.H. Freeman Co., San Francisco, CA (1969); Merrifield, J. Am. Chem. Soc., 85:2149-2154 (1963)]. *In vitro* protein synthesis may be performed using 10 manual techniques or by automation. Automated synthesis may be accomplished, for instance, using an Applied Biosystems Peptide Synthesizer (Foster City, CA) using manufacturer's instructions. Various portions of the PRO may be chemically synthesized separately and combined using chemical or enzymatic methods to produce the full-length PRO.

##### 1. Isolation of DNA Encoding PRO

15 DNA encoding PRO may be obtained from a cDNA library prepared from tissue believed to possess the PRO mRNA and to express it at a detectable level. Accordingly, human PRO DNA can be conveniently obtained from a cDNA library prepared from human tissue, such as described in the Examples. The PRO-encoding gene may also be obtained from a genomic library or by known synthetic procedures (e.g., automated nucleic acid synthesis).

20 Libraries can be screened with probes (such as antibodies to the PRO or oligonucleotides of at least about 20-80 bases) designed to identify the gene of interest or the protein encoded by it. Screening the cDNA or genomic library with the selected probe may be conducted using standard procedures, such as described in Sambrook et al., Molecular Cloning: A Laboratory Manual (New York: Cold Spring Harbor Laboratory Press, 1989). An alternative means to isolate the gene encoding PRO is to use PCR methodology 25 [Sambrook et al., supra; Dieffenbach et al., PCR Primer: A Laboratory Manual (Cold Spring Harbor Laboratory Press, 1995)].

30 The Examples below describe techniques for screening a cDNA library. The oligonucleotide sequences selected as probes should be of sufficient length and sufficiently unambiguous that false positives are minimized. The oligonucleotide is preferably labeled such that it can be detected upon hybridization to DNA in the library being screened. Methods of labeling are well known in the art, and include the use of radiolabels like <sup>32</sup>P-labeled ATP, biotinylation or enzyme labeling. Hybridization conditions, including moderate stringency and high stringency, are provided in Sambrook et al., supra.

35 Sequences identified in such library screening methods can be compared and aligned to other known sequences deposited and available in public databases such as GenBank or other private sequence databases. Sequence identity (at either the amino acid or nucleotide level) within defined regions of the molecule or across the full-length sequence can be determined using methods known in the art and as described herein.

Nucleic acid having protein coding sequence may be obtained by screening selected cDNA or genomic libraries using the deduced amino acid sequence disclosed herein for the first time, and, if

necessary, using conventional primer extension procedures as described in Sambrook et al., supra, to detect precursors and processing intermediates of mRNA that may not have been reverse-transcribed into cDNA.

## 2. Selection and Transformation of Host Cells

5 Host cells are transfected or transformed with expression or cloning vectors described herein for PRO production and cultured in conventional nutrient media modified as appropriate for inducing promoters, selecting transformants, or amplifying the genes encoding the desired sequences. The culture conditions, such as media, temperature, pH and the like, can be selected by the skilled artisan without undue experimentation. In general, principles, protocols, and practical techniques for maximizing the productivity  
10 of cell cultures can be found in Mammalian Cell Biotechnology: a Practical Approach, M. Butler, ed. (IRL Press, 1991) and Sambrook et al., supra.

Methods of eukaryotic cell transfection and prokaryotic cell transformation are known to the ordinarily skilled artisan, for example, CaCl<sub>2</sub>, CaPO<sub>4</sub>, liposome-mediated and electroporation. Depending on the host cell used, transformation is performed using standard techniques appropriate to such cells. The  
15 calcium treatment employing calcium chloride, as described in Sambrook et al., supra, or electroporation is generally used for prokaryotes. Infection with *Agrobacterium tumefaciens* is used for transformation of certain plant cells, as described by Shaw et al., Gene, 23:315 (1983) and WO 89/05859 published 29 June 1989. For mammalian cells without such cell walls, the calcium phosphate precipitation method of Graham and van der Eb, Virology, 52:456-457 (1978) can be employed. General aspects of mammalian cell host  
20 system transfections have been described in U.S. Patent No. 4,399,216. Transformations into yeast are typically carried out according to the method of Van Solingen et al., J. Bact., 130:946 (1977) and Hsiao et al., Proc. Natl. Acad. Sci. (USA), 76:3829 (1979). However, other methods for introducing DNA into cells, such as by nuclear microinjection, electroporation, bacterial protoplast fusion with intact cells, or polycations, e.g., polybrene, polyornithine, may also be used. For various techniques for transforming  
25 mammalian cells, see Keown et al., Methods in Enzymology, 185:527-537 (1990) and Mansour et al., Nature, 336:348-352 (1988).

Suitable host cells for cloning or expressing the DNA in the vectors herein include prokaryote, yeast, or higher eukaryote cells. Suitable prokaryotes include but are not limited to eubacteria, such as Gram-negative or Gram-positive organisms, for example, Enterobacteriaceae such as *E. coli*. Various *E. coli* strains are publicly available, such as *E. coli* K12 strain MM294 (ATCC 31,446); *E. coli* X1776 (ATCC 31,537); *E. coli* strain W3110 (ATCC 27,325) and K5 772 (ATCC 53,635). Other suitable prokaryotic host cells include Enterobacteriaceae such as *Escherichia*, e.g., *E. coli*, *Enterobacter*, *Erwinia*, *Klebsiella*, *Proteus*, *Salmonella*, e.g., *Salmonella typhimurium*, *Serratia*, e.g., *Serratia marcescans*, and *Shigella*, as well as *Bacilli* such as *B. subtilis* and *B. licheniformis* (e.g., *B. licheniformis* 41P disclosed in DD 266,710 published 12 April 1989), *Pseudomonas* such as *P. aeruginosa*, and *Streptomyces*. These examples are illustrative rather than limiting. Strain W3110 is one particularly preferred host or parent host because it is a common host strain for recombinant DNA product fermentations. Preferably, the host cell secretes minimal amounts of proteolytic enzymes. For example, strain W3110 may be modified to effect a genetic mutation in the genes encoding proteins endogenous to the host, with examples of such hosts including *E. coli* W3110  
40 strain 1A2, which has the complete genotype *tonA*; *E. coli* W3110 strain 9E4, which has the complete

genotype *tonA ptr3*; *E. coli* W3110 strain 27C7 (ATCC 55,244), which has the complete genotype *tonA ptr3 phoA E15 (argF-lac)169 degP ompT kan'*; *E. coli* W3110 strain 37D6, which has the complete genotype *tonA ptr3 phoA E15 (argF-lac)169 degP ompT rbs7 ilvG kan'*; *E. coli* W3110 strain 40B4, which is strain 37D6 with a non-kanamycin resistant *degP* deletion mutation; and an *E. coli* strain having mutant 5 periplasmic protease disclosed in U.S. Patent No. 4,946,783 issued 7 August 1990. Alternatively, *in vitro* methods of cloning, e.g., PCR or other nucleic acid polymerase reactions, are suitable.

In addition to prokaryotes, eukaryotic microbes such as filamentous fungi or yeast are suitable cloning or expression hosts for PRO-encoding vectors. *Saccharomyces cerevisiae* is a commonly used lower eukaryotic host microorganism. Others include *Schizosaccharomyces pombe* (Beach and Nurse, *Nature*, 10 290: 140 [1981]; EP 139,383 published 2 May 1985); *Kluyveromyces* hosts (U.S. Patent No. 4,943,529; Fleer et al., *Bio/Technology*, 9:968-975 (1991)) such as, e.g., *K. lactis* (MW98-8C, CBS683, CBS4574; Louvencourt et al., *J. Bacteriol.*, 154(2):737-742 [1983]), *K. fragilis* (ATCC 12,424), *K. bulgaricus* (ATCC 16,045), *K. wickeramii* (ATCC 24,178), *K. waltii* (ATCC 56,500), *K. drosophilae* (ATCC 36,906; Van den Berg et al., *Bio/Technology*, 8:135 (1990)), *K. thermotolerans*, and *K. marxianus*; *yarrowia* (EP 15 402,226); *Pichia pastoris* (EP 183,070; Sreekrishna et al., *J. Basic Microbiol.*, 28:265-278 [1988]); *Candida*; *Trichoderma reesia* (EP 244,234); *Neurospora crassa* (Case et al., *Proc. Natl. Acad. Sci. USA*, 76:5259-5263 [1979]); *Schwanniomyces* such as *Schwanniomyces occidentalis* (EP 394,538 published 31 October 1990); and filamentous fungi such as, e.g., *Neurospora*, *Penicillium*, *Tolypocladium* (WO 91/00357 published 10 January 1991), and *Aspergillus* hosts such as *A. nidulans* (Ballance et al., *Biochem. Biophys. Res. Commun.*, 112:284-289 [1983]; Tilburn et al., *Gene*, 26:205-221 [1983]; Yelton et al., *Proc. Natl. Acad. Sci. USA*, 81: 1470-1474 [1984]) and *A. niger* (Kelly and Hynes, *EMBO J.*, 4:475-479 [1985]). Methylotropic yeasts are suitable herein and include, but are not limited to, yeast capable of growth on methanol selected from the genera consisting of *Hansenula*, *Candida*, *Kloeckera*, *Pichia*, *Saccharomyces*, *Torulopsis*, and *Rhodotorula*. A list of specific species that are exemplary of this class of yeasts may be 20 found in C. Anthony, *The Biochemistry of Methylotrophs*, 269 (1982).

Suitable host cells for the expression of glycosylated PRO are derived from multicellular organisms. Examples of invertebrate cells include insect cells such as *Drosophila S2* and *Spodoptera Sf9*, as well as plant cells. Examples of useful mammalian host cell lines include Chinese hamster ovary (CHO) and COS cells. More specific examples include monkey kidney CV1 line transformed by SV40 (COS-7, ATCC 30 CRL 1651); human embryonic kidney line (293 or 293 cells subcloned for growth in suspension culture, Graham et al., *J. Gen Virol.*, 36:59 (1977)); Chinese hamster ovary cells/-DHFR (CHO, Urlaub and Chasin, *Proc. Natl. Acad. Sci. USA*, 77:4216 (1980)); mouse sertoli cells (TM4, Mather, *Biol. Reprod.*, 23:243-251 (1980)); human lung cells (W138, ATCC CCL 75); human liver cells (Hep G2, HB 8065); and mouse mammary tumor (MMT 060562, ATCC CCL51). The selection of the appropriate host cell is deemed to be 35 within the skill in the art.

### 3. Selection and Use of a Replicable Vector

The nucleic acid (e.g., cDNA or genomic DNA) encoding PRO may be inserted into a replicable vector for cloning (amplification of the DNA) or for expression. Various vectors are publicly available. The vector may, for example, be in the form of a plasmid, cosmid, viral particle, or phage. The appropriate 40 nucleic acid sequence may be inserted into the vector by a variety of procedures. In general, DNA is

inserted into an appropriate restriction endonuclease site(s) using techniques known in the art. Vector components generally include, but are not limited to, one or more of a signal sequence, an origin of replication, one or more marker genes, an enhancer element, a promoter, and a transcription termination sequence. Construction of suitable vectors containing one or more of these components employs standard ligation techniques which are known to the skilled artisan.

The PRO may be produced recombinantly not only directly, but also as a fusion polypeptide with a heterologous polypeptide, which may be a signal sequence or other polypeptide having a specific cleavage site at the N-terminus of the mature protein or polypeptide. In general, the signal sequence may be a component of the vector, or it may be a part of the PRO-encoding DNA that is inserted into the vector. The signal sequence may be a prokaryotic signal sequence selected, for example, from the group of the alkaline phosphatase, penicillinase, Ipp, or heat-stable enterotoxin II leaders. For yeast secretion the signal sequence may be, e.g., the yeast invertase leader, alpha factor leader (including *Saccharomyces* and *Kluyveromyces* α-factor leaders, the latter described in U.S. Patent No. 5,010,182), or acid phosphatase leader, the *C. albicans* glucoamylase leader (EP 362,179 published 4 April 1990), or the signal described in WO 90/13646 published 15 November 1990. In mammalian cell expression, mammalian signal sequences may be used to direct secretion of the protein, such as signal sequences from secreted polypeptides of the same or related species, as well as viral secretory leaders.

Both expression and cloning vectors contain a nucleic acid sequence that enables the vector to replicate in one or more selected host cells. Such sequences are well known for a variety of bacteria, yeast, and viruses. The origin of replication from the plasmid pBR322 is suitable for most Gram-negative bacteria, the 2μ plasmid origin is suitable for yeast, and various viral origins (SV40, polyoma, adenovirus, VSV or BPV) are useful for cloning vectors in mammalian cells.

Expression and cloning vectors will typically contain a selection gene, also termed a selectable marker. Typical selection genes encode proteins that (a) confer resistance to antibiotics or other toxins, e.g., ampicillin, neomycin, methotrexate, or tetracycline, (b) complement auxotrophic deficiencies, or (c) supply critical nutrients not available from complex media, e.g., the gene encoding D-alanine racemase for *Bacilli*.

An example of suitable selectable markers for mammalian cells are those that enable the identification of cells competent to take up the PRO-encoding nucleic acid, such as DHFR or thymidine kinase. An appropriate host cell when wild-type DHFR is employed is the CHO cell line deficient in DHFR activity, prepared and propagated as described by Urlaub et al., *Proc. Natl. Acad. Sci. USA*, 77:4216 (1980). A suitable selection gene for use in yeast is the *trp1* gene present in the yeast plasmid YRp7 [Stinchcomb et al., *Nature*, 282:39 (1979); Kingsman et al., *Gene*, 7:141 (1979); Tschemper et al., *Gene*, 10:157 (1980)]. The *trp1* gene provides a selection marker for a mutant strain of yeast lacking the ability to grow in tryptophan, for example, ATCC No. 44076 or PEP4-1 [Jones, *Genetics*, 85:12 (1977)].

Expression and cloning vectors usually contain a promoter operably linked to the PRO-encoding nucleic acid sequence to direct mRNA synthesis. Promoters recognized by a variety of potential host cells are well known. Promoters suitable for use with prokaryotic hosts include the β-lactamase and lactose promoter systems [Chang et al., *Nature*, 275:615 (1978); Goeddel et al., *Nature*, 281:544 (1979)], alkaline phosphatase, a tryptophan (*trp*) promoter system [Goeddel, *Nucleic Acids Res.*, 8:4057 (1980); EP 36,776], and hybrid promoters such as the tac promoter [deBoer et al., *Proc. Natl. Acad. Sci. USA*, 80:21-25 (1983)].

Promoters for use in bacterial systems also will contain a Shine-Dalgarno (S.D.) sequence operably linked to the DNA encoding PRO.

Examples of suitable promoting sequences for use with yeast hosts include the promoters for 3-phosphoglycerate kinase [Hitzeman et al., *J. Biol. Chem.*, 255:2073 (1980)] or other glycolytic enzymes [Hess et al., *J. Adv. Enzyme Reg.*, 7:149 (1968); Holland, *Biochemistry*, 17:4900 (1978)], such as enolase, glyceraldehyde-3-phosphate dehydrogenase, hexokinase, pyruvate decarboxylase, phosphofructokinase, glucose-6-phosphate isomerase, 3-phosphoglycerate mutase, pyruvate kinase, triosephosphate isomerase, phosphoglucose isomerase, and glucokinase.

Other yeast promoters, which are inducible promoters having the additional advantage of transcription controlled by growth conditions, are the promoter regions for alcohol dehydrogenase 2, isocytochrome C, acid phosphatase, degradative enzymes associated with nitrogen metabolism, metallothionein, glyceraldehyde-3-phosphate dehydrogenase, and enzymes responsible for maltose and galactose utilization. Suitable vectors and promoters for use in yeast expression are further described in EP 73,657.

PRO transcription from vectors in mammalian host cells is controlled, for example, by promoters obtained from the genomes of viruses such as polyoma virus, fowlpox virus (UK 2,211,504 published 5 July 1989), adenovirus (such as Adenovirus 2), bovine papilloma virus, avian sarcoma virus, cytomegalovirus, a retrovirus, hepatitis-B virus and Simian Virus 40 (SV40), from heterologous mammalian promoters, e.g., the actin promoter or an immunoglobulin promoter, and from heat-shock promoters, provided such promoters are compatible with the host cell systems.

Transcription of a DNA encoding the PRO by higher eukaryotes may be increased by inserting an enhancer sequence into the vector. Enhancers are cis-acting elements of DNA, usually about from 10 to 300 bp, that act on a promoter to increase its transcription. Many enhancer sequences are now known from mammalian genes (globin, elastase, albumin,  $\alpha$ -fetoprotein, and insulin). Typically, however, one will use an enhancer from a eukaryotic cell virus. Examples include the SV40 enhancer on the late side of the replication origin (bp 100-270), the cytomegalovirus early promoter enhancer, the polyoma enhancer on the late side of the replication origin, and adenovirus enhancers. The enhancer may be spliced into the vector at a position 5' or 3' to the PRO coding sequence, but is preferably located at a site 5' from the promoter.

Expression vectors used in eukaryotic host cells (yeast, fungi, insect, plant, animal, human, or nucleated cells from other multicellular organisms) will also contain sequences necessary for the termination of transcription and for stabilizing the mRNA. Such sequences are commonly available from the 5' and, occasionally 3', untranslated regions of eukaryotic or viral DNAs or cDNAs. These regions contain nucleotide segments transcribed as polyadenylated fragments in the untranslated portion of the mRNA encoding PRO.

Still other methods, vectors, and host cells suitable for adaptation to the synthesis of PRO in recombinant vertebrate cell culture are described in Gething et al., *Nature*, 293:620-625 (1981); Mantei et al., *Nature*, 281:40-46 (1979); EP 117,060; and EP 117,058.

#### 4. Detecting Gene Amplification/Expression

Gene amplification and/or expression may be measured in a sample directly, for example, by conventional Southern blotting, Northern blotting to quantitate the transcription of mRNA [Thomas, *Proc.*

Natl. Acad. Sci. USA, 77:5201-5205 (1980)], dot blotting (DNA analysis), or *in situ* hybridization, using an appropriately labeled probe, based on the sequences provided herein. Alternatively, antibodies may be employed that can recognize specific duplexes, including DNA duplexes, RNA duplexes, and DNA-RNA hybrid duplexes or DNA-protein duplexes. The antibodies in turn may be labeled and the assay may be 5 carried out where the duplex is bound to a surface, so that upon the formation of duplex on the surface, the presence of antibody bound to the duplex can be detected.

Gene expression, alternatively, may be measured by immunological methods, such as immunohistochemical staining of cells or tissue sections and assay of cell culture or body fluids, to quantitate directly the expression of gene product. Antibodies useful for immunohistochemical staining 10 and/or assay of sample fluids may be either monoclonal or polyclonal, and may be prepared in any mammal. Conveniently, the antibodies may be prepared against a native sequence PRO polypeptide or against a synthetic peptide based on the DNA sequences provided herein or against exogenous sequence fused to PRO DNA and encoding a specific antibody epitope.

#### 5. Purification of Polypeptide

Forms of PRO may be recovered from culture medium or from host cell lysates. If membrane-bound, it can be released from the membrane using a suitable detergent solution (e.g. Triton-X 100) or by enzymatic cleavage. Cells employed in expression of PRO can be disrupted by various physical or chemical means, such as freeze-thaw cycling, sonication, mechanical disruption, or cell lysing agents.

It may be desired to purify PRO from recombinant cell proteins or polypeptides. The following 20 procedures are exemplary of suitable purification procedures: by fractionation on an ion-exchange column; ethanol precipitation; reverse phase HPLC; chromatography on silica or on a cation-exchange resin such as DEAE; chromatofocusing; SDS-PAGE; ammonium sulfate precipitation; gel filtration using, for example, Sephadex G-75; protein A Sepharose columns to remove contaminants such as IgG; and metal chelating 25 columns to bind epitope-tagged forms of the PRO. Various methods of protein purification may be employed and such methods are known in the art and described for example in Deutscher, Methods in Enzymology, 182 (1990); Scopes, Protein Purification: Principles and Practice, Springer-Verlag, New York (1982). The purification step(s) selected will depend, for example, on the nature of the production process used and the particular PRO produced.

#### E. Tissue Distribution

The location of tissues expressing the PRO can be identified by determining mRNA expression in 30 various human tissues. The location of such genes provides information about which tissues are most likely to be affected by the stimulating and inhibiting activities of the PRO polypeptides. The location of a gene in a specific tissue also provides sample tissue for the activity blocking assays discussed below.

As noted before, gene expression in various tissues may be measured by conventional Southern blotting, Northern blotting to quantitate the transcription of mRNA (Thomas, *Proc. Natl. Acad. Sci. USA*, 77:5201-5205 [1980]), dot blotting (DNA analysis), or *in situ* hybridization, using an appropriately labeled probe, based on the sequences provided herein. Alternatively, antibodies may be employed that can recognize specific duplexes, including DNA duplexes, RNA duplexes, and DNA-RNA hybrid duplexes or DNA-protein duplexes.

40 Gene expression in various tissues, alternatively, may be measured by immunological methods,

such as immunohistochemical staining of tissue sections and assay of cell culture or body fluids, to quantitate directly the expression of gene product. Antibodies useful for immunohistochemical staining and/or assay of sample fluids may be either monoclonal or polyclonal, and may be prepared in any mammal. Conveniently, the antibodies may be prepared against a native sequence of a PRO polypeptide or against a 5 synthetic peptide based on the DNA sequences encoding the PRO polypeptide or against an exogenous sequence fused to a DNA encoding a PRO polypeptide and encoding a specific antibody epitope. General techniques for generating antibodies, and special protocols for Northern blotting and *in situ* hybridization are provided below.

F. Antibody Binding Studies

10 The activity of the PRO polypeptides can be further verified by antibody binding studies, in which the ability of anti-PRO antibodies to inhibit the effect of the PRO polypeptides, respectively, on tissue cells is tested. Exemplary antibodies include polyclonal, monoclonal, humanized, bispecific, and heteroconjugate antibodies, the preparation of which will be described hereinbelow.

15 Antibody binding studies may be carried out in any known assay method, such as competitive binding assays, direct and indirect sandwich assays, and immunoprecipitation assays. Zola, *Monoclonal Antibodies: A Manual of Techniques*, pp.147-158 (CRC Press, Inc., 1987).

20 Competitive binding assays rely on the ability of a labeled standard to compete with the test sample analyte for binding with a limited amount of antibody. The amount of target protein in the test sample is inversely proportional to the amount of standard that becomes bound to the antibodies. To facilitate determining the amount of standard that becomes bound, the antibodies preferably are insolubilized before or after the competition, so that the standard and analyte that are bound to the antibodies may conveniently be separated from the standard and analyte which remain unbound.

25 Sandwich assays involve the use of two antibodies, each capable of binding to a different immunogenic portion, or epitope, of the protein to be detected. In a sandwich assay, the test sample analyte is bound by a first antibody which is immobilized on a solid support, and thereafter a second antibody binds to the analyte, thus forming an insoluble three-part complex. See, e.g., US Pat No. 4,376,110. The second antibody may itself be labeled with a detectable moiety (direct sandwich assays) or may be measured using an anti-immunoglobulin antibody that is labeled with a detectable moiety (indirect sandwich assay). For example, one type of sandwich assay is an ELISA assay, in which case the detectable moiety is an enzyme.

30 For immunohistochemistry, the tissue sample may be fresh or frozen or may be embedded in paraffin and fixed with a preservative such as formalin, for example.

G. Cell-Based Assays

35 Cell-based assays and animal models for immune related diseases can be used to further understand the relationship between the genes and polypeptides identified herein and the development and pathogenesis of immune related disease.

40 In a different approach, cells of a cell type known to be involved in a particular immune related disease are transfected with the cDNAs described herein, and the ability of these cDNAs to stimulate or inhibit immune function is analyzed. Suitable cells can be transfected with the desired gene, and monitored for immune function activity. Such transfected cell lines can then be used to test the ability of poly- or monoclonal antibodies or antibody compositions to inhibit or stimulate immune function, for example to

modulate T-cell proliferation or inflammatory cell infiltration. Cells transfected with the coding sequences of the genes identified herein can further be used to identify drug candidates for the treatment of immune related diseases.

In addition, primary cultures derived from transgenic animals (as described below) can be used in 5 the cell-based assays herein, although stable cell lines are preferred. Techniques to derive continuous cell lines from transgenic animals are well known in the art (see, e.g., Small *et al.*, *Mol. Cell. Biol.* 5: 642-648 [1985]).

One suitable cell based assay is the mixed lymphocyte reaction (MLR). *Current Protocols in Immunology*, unit 3.12; edited by J E Coligan, A M Kruisbeek, D H Marglies, E M Shevach, W Strober, 10 National Institutes of Health, Published by John Wiley & Sons, Inc. In this assay, the ability of a test compound to stimulate or inhibit the proliferation of activated T cells is assayed. A suspension of responder T cells is cultured with allogeneic stimulator cells and the proliferation of T cells is measured by uptake of tritiated thymidine. This assay is a general measure of T cell reactivity. Since the majority of T cells respond to and produce IL-2 upon activation, differences in responsiveness in this assay in part reflect 15 differences in IL-2 production by the responding cells. The MLR results can be verified by a standard lymphokine (IL-2) detection assay. *Current Protocols in Immunology*, above, 3.15, 6.3.

A proliferative T cell response in an MLR assay may be due to direct mitogenic properties of an assayed molecule or to external antigen induced activation. Additional verification of the T cell stimulatory activity of the PRO polypeptides can be obtained by a costimulation assay. T cell activation requires an 20 antigen specific signal mediated through the T-cell receptor (TCR) and a costimulatory signal mediated through a second ligand binding interaction, for example, the B7 (CD80, CD86)/CD28 binding interaction. CD28 crosslinking increases lymphokine secretion by activated T cells. T cell activation has both negative and positive controls through the binding of ligands which have a negative or positive effect. CD28 and CTLA-4 are related glycoproteins in the Ig superfamily which bind to B7. CD28 binding to B7 has a 25 positive costimulation effect of T cell activation; conversely, CTLA-4 binding to B7 has a T cell deactivating effect. Chambers, C. A. and Allison, J. P., *Curr. Opin. Immunol.* (1997) 9:396. Schwartz, R. H., *Cell* (1992) 71:1065; Linsey, P. S. and Ledbetter, J. A., *Annu. Rev. Immunol.* (1993) 11:191; June, C. H. *et al*, *Immunol. Today* (1994) 15:321; Jenkins, M. K., *Immunity* (1994) 1:405. In a costimulation assay, the PRO polypeptides are assayed for T cell costimulatory or inhibitory activity.

30 Direct use of a stimulating compound as in the invention has been validated in experiments with 4-1BB glycoprotein, a member of the tumor necrosis factor receptor family, which binds to a ligand (4-1BBL) expressed on primed T cells and signals T cell activation and growth. Alderson, M. E. *et al.*, *J. Immunol.* (1994) 24:2219.

The use of an agonist stimulating compound has also been validated experimentally. Activation of 35 4-1BB by treatment with an agonist anti-4-1BB antibody enhances eradication of tumors. Hellstrom, I. and Hellstrom, K. E., *Crit. Rev. Immunol.* (1998) 18:1. Immunoadjuvant therapy for treatment of tumors, described in more detail below, is another example of the use of the stimulating compounds of the invention.

40 Alternatively, an immune stimulating or enhancing effect can also be achieved by administration of a PRO which has vascular permeability enhancing properties. Enhanced vascular permeability would be

beneficial to disorders which can be attenuated by local infiltration of immune cells (*e.g.*, monocytes, eosinophils, PMNs) and inflammation.

On the other hand, PRO polypeptides, as well as other compounds of the invention, which are direct inhibitors of T cell proliferation/activation, lymphokine secretion, and/or vascular permeability can be directly used to suppress the immune response. These compounds are useful to reduce the degree of the immune response and to treat immune related diseases characterized by a hyperactive, superoptimal, or autoimmune response. This use of the compounds of the invention has been validated by the experiments described above in which CTLA-4 binding to receptor B7 deactivates T cells. The direct inhibitory compounds of the invention function in an analogous manner. The use of compound which suppress vascular permeability would be expected to reduce inflammation. Such uses would be beneficial in treating conditions associated with excessive inflammation.

Alternatively, compounds, *e.g.*, antibodies, which bind to stimulating PRO polypeptides and block the stimulating effect of these molecules produce a net inhibitory effect and can be used to suppress the T cell mediated immune response by inhibiting T cell proliferation/activation and/or lymphokine secretion. Blocking the stimulating effect of the polypeptides suppresses the immune response of the mammal. This use has been validated in experiments using an anti-IL2 antibody. In these experiments, the antibody binds to IL2 and blocks binding of IL2 to its receptor thereby achieving a T cell inhibitory effect.

#### H. Animal Models

The results of the cell based *in vitro* assays can be further verified using *in vivo* animal models and assays for T-cell function. A variety of well known animal models can be used to further understand the role of the genes identified herein in the development and pathogenesis of immune related disease, and to test the efficacy of candidate therapeutic agents, including antibodies, and other antagonists of the native polypeptides, including small molecule antagonists. The *in vivo* nature of such models makes them predictive of responses in human patients. Animal models of immune related diseases include both non-recombinant and recombinant (transgenic) animals. Non-recombinant animal models include, for example, rodent, *e.g.*, murine models. Such models can be generated by introducing cells into syngeneic mice using standard techniques, *e.g.*, subcutaneous injection, tail vein injection, spleen implantation, intraperitoneal implantation, implantation under the renal capsule, *etc.*

Graft-versus-host disease occurs when immunocompetent cells are transplanted into immunosuppressed or tolerant patients. The donor cells recognize and respond to host antigens. The response can vary from life threatening severe inflammation to mild cases of diarrhea and weight loss. Graft-versus-host disease models provide a means of assessing T cell reactivity against MHC antigens and minor transplant antigens. A suitable procedure is described in detail in Current Protocols in Immunology, above, unit 4.3.

An animal model for skin allograft rejection is a means of testing the ability of T cells to mediate *in vivo* tissue destruction and a measure of their role in transplant rejection. The most common and accepted models use murine tail-skin grafts. Repeated experiments have shown that skin allograft rejection is mediated by T cells, helper T cells and killer-effector T cells, and not antibodies. Auchincloss, H. Jr. and Sachs, D. H., *Fundamental Immunology*, 2nd ed., W. E. Paul ed., Raven Press, NY, 1989, 889-992. A suitable procedure is described in detail in *Current Protocols in Immunology*, above, unit 4.4. Other

transplant rejection models which can be used to test the compounds of the invention are the allogeneic heart transplant models described by Tanabe, M. *et al.*, *Transplantation* (1994) 58:23 and Tinubu, S. A. *et al.*, *J. Immunol.* (1994) 4330-4338.

5 Animal models for delayed type hypersensitivity provides an assay of cell mediated immune function as well. Delayed type hypersensitivity reactions are a T cell mediated *in vivo* immune response characterized by inflammation which does not reach a peak until after a period of time has elapsed after challenge with an antigen. These reactions also occur in tissue specific autoimmune diseases such as multiple sclerosis (MS) and experimental autoimmune encephalomyelitis (EAE, a model for MS). A suitable procedure is described in detail in *Current Protocols in Immunology*, above, unit 4.5.

10 EAE is a T cell mediated autoimmune disease characterized by T cell and mononuclear cell inflammation and subsequent demyelination of axons in the central nervous system. EAE is generally considered to be a relevant animal model for MS in humans. Bolton, C., *Multiple Sclerosis* (1995) 1:143. Both acute and relapsing-remitting models have been developed. The compounds of the invention can be tested for T cell stimulatory or inhibitory activity against immune mediated demyelinating disease using the 15 protocol described in *Current Protocols in Immunology*, above, units 15.1 and 15.2. See also the models for myelin disease in which oligodendrocytes or Schwann cells are grafted into the central nervous system as described in Duncan, I. D. *et al.*, *Molec. Med. Today* (1997) 554-561.

20 Contact hypersensitivity is a simple delayed type hypersensitivity *in vivo* assay of cell mediated immune function. In this procedure, cutaneous exposure to exogenous haptens which gives rise to a delayed type hypersensitivity reaction which is measured and quantitated. Contact sensitivity involves an initial sensitizing phase followed by an elicitation phase. The elicitation phase occurs when the T lymphocytes encounter an antigen to which they have had previous contact. Swelling and inflammation occur, making this an excellent model of human allergic contact dermatitis. A suitable procedure is described in detail in 25 *Current Protocols in Immunology*, Eds. J. E. Cologan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach and W. Strober, John Wiley & Sons, Inc., 1994, unit 4.2. See also Grabbe, S. and Schwarz, T, *Immun. Today* 19 (1): 37-44 (1998).

30 An animal model for arthritis is collagen-induced arthritis. This model shares clinical, histological and immunological characteristics of human autoimmune rheumatoid arthritis and is an acceptable model for human autoimmune arthritis. Mouse and rat models are characterized by synovitis, erosion of cartilage and subchondral bone. The compounds of the invention can be tested for activity against autoimmune arthritis using the protocols described in *Current Protocols in Immunology*, above, units 15.5. See also the model using a monoclonal antibody to CD18 and VLA-4 integrins described in Issekutz, A.C. *et al.*, *Immunology* (1996) 88:569.

35 A model of asthma has been described in which antigen-induced airway hyper-reactivity, pulmonary eosinophilia and inflammation are induced by sensitizing an animal with ovalbumin and then challenging the animal with the same protein delivered by aerosol. Several animal models (guinea pig, rat, non-human primate) show symptoms similar to atopic asthma in humans upon challenge with aerosol antigens. Murine models have many of the features of human asthma. Suitable procedures to test the 40 compounds of the invention for activity and effectiveness in the treatment of asthma are described by Wolyniec, W. W. *et al.*, *Am. J. Respir. Cell Mol. Biol.* (1998) 18:777 and the references cited therein.

Additionally, the compounds of the invention can be tested on animal models for psoriasis like diseases. Evidence suggests a T cell pathogenesis for psoriasis. The compounds of the invention can be tested in the scid/scid mouse model described by Schon, M. P. *et al*, *Nat. Med.* (1997) 3:183, in which the mice demonstrate histopathologic skin lesions resembling psoriasis. Another suitable model is the human skin/scid mouse chimera prepared as described by Nickoloff, B. J. *et al*, *Am. J. Path.* (1995) 146:580.

Recombinant (transgenic) animal models can be engineered by introducing the coding portion of the genes identified herein into the genome of animals of interest, using standard techniques for producing transgenic animals. Animals that can serve as a target for transgenic manipulation include, without limitation, mice, rats, rabbits, guinea pigs, sheep, goats, pigs, and non-human primates, *e.g.*, baboons, chimpanzees and monkeys. Techniques known in the art to introduce a transgene into such animals include pronucleic microinjection (Hoppe and Wanger, U.S. Patent No. 4,873,191); retrovirus-mediated gene transfer into germ lines (*e.g.*, Van der Putten *et al*, *Proc. Natl. Acad. Sci. USA* 82, 6148-615 [1985]); gene targeting in embryonic stem cells (Thompson *et al*, *Cell* 56, 313-321 [1989]); electroporation of embryos (Lo, *Mol. Cel. Biol.* 3, 1803-1814 [1983]); sperm-mediated gene transfer (Lavitrano *et al*, *Cell* 57, 717-73 [1989]). For review, see, for example, U.S. Patent No. 4,736,866.

For the purpose of the present invention, transgenic animals include those that carry the transgene only in part of their cells ("mosaic animals"). The transgene can be integrated either as a single transgene, or in concatamers, *e.g.*, head-to-head or head-to-tail tandems. Selective introduction of a transgene into a particular cell type is also possible by following, for example, the technique of Lasko *et al*, *Proc. Natl. Acad. Sci. USA* 89, 6232-636 (1992).

The expression of the transgene in transgenic animals can be monitored by standard techniques. For example, Southern blot analysis or PCR amplification can be used to verify the integration of the transgene. The level of mRNA expression can then be analyzed using techniques such as *in situ* hybridization, Northern blot analysis, PCR, or immunocytochemistry.

The animals may be further examined for signs of immune disease pathology, for example by histological examination to determine infiltration of immune cells into specific tissues. Blocking experiments can also be performed in which the transgenic animals are treated with the compounds of the invention to determine the extent of the T cell proliferation stimulation or inhibition of the compounds. In these experiments, blocking antibodies which bind to the PRO polypeptide, prepared as described above, are administered to the animal and the effect on immune function is determined.

Alternatively, "knock out" animals can be constructed which have a defective or altered gene encoding a polypeptide identified herein, as a result of homologous recombination between the endogenous gene encoding the polypeptide and altered genomic DNA encoding the same polypeptide introduced into an embryonic cell of the animal. For example, cDNA encoding a particular polypeptide can be used to clone genomic DNA encoding that polypeptide in accordance with established techniques. A portion of the genomic DNA encoding a particular polypeptide can be deleted or replaced with another gene, such as a gene encoding a selectable marker which can be used to monitor integration. Typically, several kilobases of unaltered flanking DNA (both at the 5' and 3' ends) are included in the vector [*see e.g.*, Thomas and Capecchi, *Cell*, 51:503 (1987) for a description of homologous recombination vectors]. The vector is introduced into an embryonic stem cell line (*e.g.*, by electroporation) and cells in which the introduced DNA

has homologously recombined with the endogenous DNA are selected [see e.g., Li *et al.*, *Cell*, 69:915 (1992)]. The selected cells are then injected into a blastocyst of an animal (e.g., a mouse or rat) to form aggregation chimeras [see e.g., Bradley, in *Teratocarcinomas and Embryonic Stem Cells: A Practical Approach*, E. J. Robertson, ed. (IRL, Oxford, 1987), pp. 113-152]. A chimeric embryo can then be  
5 implanted into a suitable pseudopregnant female foster animal and the embryo brought to term to create a "knock out" animal. Progeny harboring the homologously recombined DNA in their germ cells can be identified by standard techniques and used to breed animals in which all cells of the animal contain the homologously recombined DNA. Knockout animals can be characterized for instance, for their ability to defend against certain pathological conditions and for their development of pathological conditions due to  
10 absence of the polypeptide.

I. ImmunoAdjuvant Therapy

In one embodiment, the immunostimulating compounds of the invention can be used in immunoadjuvant therapy for the treatment of tumors (cancer). It is now well established that T cells recognize human tumor specific antigens. One group of tumor antigens, encoded by the MAGE, BAGE and  
15 GAGE families of genes, are silent in all adult normal tissues , but are expressed in significant amounts in tumors, such as melanomas, lung tumors, head and neck tumors, and bladder carcinomas DeSmet *et al.*, (1996) *Proc. Natl. Acad. Sci. USA*, 93:7149. It has been shown that costimulation of T cells induces tumor regression and an antitumor response both *in vitro* and *in vivo*. Melero, I. *et al.*, *Nature Medicine* (1997)  
20 3:682; Kwon, E. D. *et al.*, *Proc. Natl. Acad. Sci. USA* (1997) 94: 8099; Lynch, D. H. *et al.*, *Nature Medicine* (1997) 3:625; Finn, O. J. and Lotze, M. T., *J. Immunol.* (1998) 21:114. The stimulatory compounds of the invention can be administered as adjuvants, alone or together with a growth regulating agent, cytotoxic agent or chemotherapeutic agent, to stimulate T cell proliferation/activation and an antitumor response to tumor antigens. The growth regulating, cytotoxic, or chemotherapeutic agent may be administered in conventional amounts using known administration regimes. Immunostimulating activity by the compounds of the  
25 invention allows reduced amounts of the growth regulating, cytotoxic, or chemotherapeutic agents thereby potentially lowering the toxicity to the patient.

J. Screening Assays for Drug Candidates

Screening assays for drug candidates are designed to identify compounds that bind to or complex with the polypeptides encoded by the genes identified herein or a biologically active fragment thereof, or  
30 otherwise interfere with the interaction of the encoded polypeptides with other cellular proteins. Such screening assays will include assays amenable to high-throughput screening of chemical libraries, making them particularly suitable for identifying small molecule drug candidates. Small molecules contemplated include synthetic organic or inorganic compounds, including peptides, preferably soluble peptides, (poly)peptide-immunoglobulin fusions, and, in particular, antibodies including, without limitation, poly- and  
35 monoclonal antibodies and antibody fragments, single-chain antibodies, anti-idiotypic antibodies, and chimeric or humanized versions of such antibodies or fragments, as well as human antibodies and antibody fragments. The assays can be performed in a variety of formats, including protein-protein binding assays, biochemical screening assays, immunoassays and cell based assays, which are well characterized in the art. All assays are common in that they call for contacting the drug candidate with a polypeptide encoded by a  
40 nucleic acid identified herein under conditions and for a time sufficient to allow these two components to

interact.

In binding assays, the interaction is binding and the complex formed can be isolated or detected in the reaction mixture. In a particular embodiment, the polypeptide encoded by the gene identified herein or the drug candidate is immobilized on a solid phase, e.g., on a microtiter plate, by covalent or non-covalent 5 attachments. Non-covalent attachment generally is accomplished by coating the solid surface with a solution of the polypeptide and drying. Alternatively, an immobilized antibody, e.g., a monoclonal antibody, specific for the polypeptide to be immobilized can be used to anchor it to a solid surface. The assay is performed by adding the non-immobilized component, which may be labeled by a detectable label, to the immobilized component, e.g., the coated surface containing the anchored component. When the reaction is complete, the 10 non-reacted components are removed, e.g., by washing, and complexes anchored on the solid surface are detected. When the originally non-immobilized component carries a detectable label, the detection of label immobilized on the surface indicates that complexing occurred. Where the originally non-immobilized component does not carry a label, complexing can be detected, for example, by using a labelled antibody specifically binding the immobilized complex.

If the candidate compound interacts with but does not bind to a particular protein encoded by a gene identified herein, its interaction with that protein can be assayed by methods well known for detecting protein-protein interactions. Such assays include traditional approaches, such as, cross-linking, co-immunoprecipitation, and co-purification through gradients or chromatographic columns. In addition, protein-protein interactions can be monitored by using a yeast-based genetic system described by Fields and 15 co-workers [Fields and Song, *Nature (London)* 340, 245-246 (1989); Chien *et al.*, *Proc. Natl. Acad. Sci. USA* 88, 9578-9582 (1991)] as disclosed by Chevray and Nathans, *Proc. Natl. Acad. Sci. USA* 89, 5789-5793 (1991). Many transcriptional activators, such as yeast GAL4, consist of two physically discrete modular domains, one acting as the DNA-binding domain, while the other one functioning as the transcription activation domain. The yeast expression system described in the foregoing publications (generally referred 20 to as the "two-hybrid system") takes advantage of this property, and employs two hybrid proteins, one in which the target protein is fused to the DNA-binding domain of GAL4, and another, in which candidate activating proteins are fused to the activation domain. The expression of a GAL1-lacZ reporter gene under control of a GAL4-activated promoter depends on reconstitution of GAL4 activity via protein-protein interaction. Colonies containing interacting polypeptides are detected with a chromogenic substrate for  $\beta$ -galactosidase. A complete kit (MATCHMAKER<sup>TM</sup>) for identifying protein-protein interactions between two 25 specific proteins using the two-hybrid technique is commercially available from Clontech. This system can also be extended to map protein domains involved in specific protein interactions as well as to pinpoint amino acid residues that are crucial for these interactions.

In order to find compounds that interfere with the interaction of a gene identified herein and other 35 intra- or extracellular components can be tested, a reaction mixture is usually prepared containing the product of the gene and the intra- or extracellular component under conditions and for a time allowing for the interaction and binding of the two products. To test the ability of a test compound to inhibit binding, the reaction is run in the absence and in the presence of the test compound. In addition, a placebo may be added to a third reaction mixture, to serve as positive control. The binding (complex formation) between the test 40 compound and the intra- or extracellular component present in the mixture is monitored as described above.

The formation of a complex in the control reaction(s) but not in the reaction mixture containing the test compound indicates that the test compound interferes with the interaction of the test compound and its reaction partner.

5           K.     Compositions and Methods for the Treatment of Immune Related Diseases

The compositions useful in the treatment of immune related diseases include, without limitation, proteins, antibodies, small organic molecules, peptides, phosphopeptides, antisense and ribozyme molecules, triple helix molecules, etc. that inhibit or stimulate immune function, for example, T cell proliferation/activation, lymphokine release, or immune cell infiltration.

For example, antisense RNA and RNA molecules act to directly block the translation of mRNA by hybridizing to targeted mRNA and preventing protein translation. When antisense DNA is used, oligodeoxyribonucleotides derived from the translation initiation site, e.g., between about -10 and +10 positions of the target gene nucleotide sequence, are preferred.

10           Ribozymes are enzymatic RNA molecules capable of catalyzing the specific cleavage of RNA. Ribozymes act by sequence-specific hybridization to the complementary target RNA, followed by 15 endonucleolytic cleavage. Specific ribozyme cleavage sites within a potential RNA target can be identified by known techniques. For further details see, e.g., Rossi, *Current Biology* 4, 469-471 (1994), and PCT publication No. WO 97/33551 (published September 18, 1997).

Nucleic acid molecules in triple helix formation used to inhibit transcription should be single-stranded and composed of deoxynucleotides. The base composition of these oligonucleotides is designed 20 such that it promotes triple helix formation via Hoogsteen base pairing rules, which generally require sizeable stretches of purines or pyrimidines on one strand of a duplex. For further details see, e.g., PCT publication No. WO 97/33551, *supra*.

These molecules can be identified by any or any combination of the screening assays discussed above and/or by any other screening techniques well known for those skilled in the art.

25           L.     Anti-PRO Antibodies

The present invention further provides anti-PRO antibodies. Exemplary antibodies include polyclonal, monoclonal, humanized, bispecific, and heteroconjugate antibodies.

1.     Polyclonal Antibodies

The anti-PRO antibodies may comprise polyclonal antibodies. Methods of preparing polyclonal 30 antibodies are known to the skilled artisan. Polyclonal antibodies can be raised in a mammal, for example, by one or more injections of an immunizing agent and, if desired, an adjuvant. Typically, the immunizing agent and/or adjuvant will be injected in the mammal by multiple subcutaneous or intraperitoneal injections. The immunizing agent may include the PRO polypeptide or a fusion protein thereof. It may be useful to conjugate the immunizing agent to a protein known to be immunogenic in the mammal being immunized. 35 Examples of such immunogenic proteins include but are not limited to keyhole limpet hemocyanin, serum albumin, bovine thyroglobulin, and soybean trypsin inhibitor. Examples of adjuvants which may be employed include Freund's complete adjuvant and MPL-TDM adjuvant (monophosphoryl Lipid A, synthetic trehalose dicorynomycolate). The immunization protocol may be selected by one skilled in the art without undue experimentation.

40           2.     Monoclonal Antibodies

The anti-PRO antibodies may, alternatively, be monoclonal antibodies. Monoclonal antibodies may be prepared using hybridoma methods, such as those described by Kohler and Milstein, Nature, 256:495 (1975). In a hybridoma method, a mouse, hamster, or other appropriate host animal, is typically immunized with an immunizing agent to elicit lymphocytes that produce or are capable of producing antibodies that will 5 specifically bind to the immunizing agent. Alternatively, the lymphocytes may be immunized *in vitro*.

The immunizing agent will typically include the PRO polypeptide or a fusion protein thereof. Generally, either peripheral blood lymphocytes ("PBLs") are used if cells of human origin are desired, or spleen cells or lymph node cells are used if non-human mammalian sources are desired. The lymphocytes are then fused with an immortalized cell line using a suitable fusing agent, such as polyethylene glycol, to 10 form a hybridoma cell [Goding, Monoclonal Antibodies: Principles and Practice, Academic Press, (1986) pp. 59-103]. Immortalized cell lines are usually transformed mammalian cells, particularly myeloma cells of rodent, bovine and human origin. Usually, rat or mouse myeloma cell lines are employed. The hybridoma 15 cells may be cultured in a suitable culture medium that preferably contains one or more substances that inhibit the growth or survival of the unfused, immortalized cells. For example, if the parental cells lack the enzyme hypoxanthine guanine phosphoribosyl transferase (HGPRT or HPRT), the culture medium for the hybridomas typically will include hypoxanthine, aminopterin, and thymidine ("HAT medium"), which substances prevent the growth of HGPRT-deficient cells.

Preferred immortalized cell lines are those that fuse efficiently, support stable high level expression of antibody by the selected antibody-producing cells, and are sensitive to a medium such as HAT medium. 20 More preferred immortalized cell lines are murine myeloma lines, which can be obtained, for instance, from the Salk Institute Cell Distribution Center, San Diego, California and the American Type Culture Collection, Manassas, Virginia. Human myeloma and mouse-human heteromyeloma cell lines also have been described for the production of human monoclonal antibodies [Kozbor, J. Immunol., 133:3001 (1984); Brodeur et al., Monoclonal Antibody Production Techniques and Applications, Marcel Dekker, Inc., New York, (1987) pp. 25 51-63].

The culture medium in which the hybridoma cells are cultured can then be assayed for the presence of monoclonal antibodies directed against PRO. Preferably, the binding specificity of monoclonal antibodies produced by the hybridoma cells is determined by immunoprecipitation or by an *in vitro* binding assay, such as radioimmunoassay (RIA) or enzyme-linked immunoabsorbent assay (ELISA). Such techniques and 30 assays are known in the art. The binding affinity of the monoclonal antibody can, for example, be determined by the Scatchard analysis of Munson and Pollard, Anal. Biochem., 107:220 (1980).

After the desired hybridoma cells are identified, the clones may be subcloned by limiting dilution procedures and grown by standard methods [Goding, supra]. Suitable culture media for this purpose include, for example, Dulbecco's Modified Eagle's Medium and RPMI-1640 medium. Alternatively, the 35 hybridoma cells may be grown *in vivo* as ascites in a mammal.

The monoclonal antibodies secreted by the subclones may be isolated or purified from the culture medium or ascites fluid by conventional immunoglobulin purification procedures such as, for example, protein A-Sepharose, hydroxylapatite chromatography, gel electrophoresis, dialysis, or affinity chromatography.

The monoclonal antibodies may also be made by recombinant DNA methods, such as those described in U.S. Patent No. 4,816,567. DNA encoding the monoclonal antibodies of the invention can be readily isolated and sequenced using conventional procedures (e.g., by using oligonucleotide probes that are capable of binding specifically to genes encoding the heavy and light chains of murine antibodies). The 5 hybridoma cells of the invention serve as a preferred source of such DNA. Once isolated, the DNA may be placed into expression vectors, which are then transfected into host cells such as simian COS cells, Chinese hamster ovary (CHO) cells, or myeloma cells that do not otherwise produce immunoglobulin protein, to obtain the synthesis of monoclonal antibodies in the recombinant host cells. The DNA also may be modified, for example, by substituting the coding sequence for human heavy and light chain constant 10 domains in place of the homologous murine sequences [U.S. Patent No. 4,816,567; Morrison et al., *supra*] or by covalently joining to the immunoglobulin coding sequence all or part of the coding sequence for a non-immunoglobulin polypeptide. Such a non-immunoglobulin polypeptide can be substituted for the constant domains of an antibody of the invention, or can be substituted for the variable domains of one antigen-combining site of an antibody of the invention to create a chimeric bivalent antibody.

15 The antibodies may be monovalent antibodies. Methods for preparing monovalent antibodies are well known in the art. For example, one method involves recombinant expression of immunoglobulin light chain and modified heavy chain. The heavy chain is truncated generally at any point in the Fc region so as to prevent heavy chain crosslinking. Alternatively, the relevant cysteine residues are substituted with another amino acid residue or are deleted so as to prevent crosslinking.

20 *In vitro* methods are also suitable for preparing monovalent antibodies. Digestion of antibodies to produce fragments thereof, particularly, Fab fragments, can be accomplished using routine techniques known in the art.

### 3. Human and Humanized Antibodies

The anti-PRO antibodies of the invention may further comprise humanized antibodies or human antibodies. Humanized forms of non-human (e.g., murine) antibodies are chimeric immunoglobulins, immunoglobulin chains or fragments thereof (such as Fv, Fab, Fab', F(ab')<sub>2</sub> or other antigen-binding subsequences of antibodies) which contain minimal sequence derived from non-human immunoglobulin. Humanized antibodies include human immunoglobulins (recipient antibody) in which residues from a complementary determining region (CDR) of the recipient are replaced by residues from a CDR of a non-human species (donor antibody) such as mouse, rat or rabbit having the desired specificity, affinity and capacity. In some instances, Fv framework residues of the human immunoglobulin are replaced by corresponding non-human residues. Humanized antibodies may also comprise residues which are found neither in the recipient antibody nor in the imported CDR or framework sequences. In general, the humanized antibody will comprise substantially all of at least one, and typically two, variable domains, in which all or substantially all of the CDR regions correspond to those of a non-human immunoglobulin and all or substantially all of the FR regions are those of a human immunoglobulin consensus sequence. The humanized antibody optimally also will comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin [Jones et al., *Nature*, 321:522-525 (1986); Riechmann et al., *Nature*, 332:323-329 (1988); and Presta, *Curr. Op. Struct. Biol.*, 2:593-596 (1992)].

Methods for humanizing non-human antibodies are well known in the art. Generally, a humanized antibody has one or more amino acid residues introduced into it from a source which is non-human. These non-human amino acid residues are often referred to as "import" residues, which are typically taken from an "import" variable domain. Humanization can be essentially performed following the method of Winter and co-workers [Jones et al., *Nature*, 321:522-525 (1986); Riechmann et al., *Nature*, 332:323-327 (1988); Verhoeyen et al., *Science*, 239:1534-1536 (1988)], by substituting rodent CDRs or CDR sequences for the corresponding sequences of a human antibody. Accordingly, such "humanized" antibodies are chimeric antibodies (U.S. Patent No. 4,816,567), wherein substantially less than an intact human variable domain has been substituted by the corresponding sequence from a non-human species. In practice, humanized antibodies are typically human antibodies in which some CDR residues and possibly some FR residues are substituted by residues from analogous sites in rodent antibodies.

Human antibodies can also be produced using various techniques known in the art, including phage display libraries [Hoogenboom and Winter, *J. Mol. Biol.*, 227:381 (1991); Marks et al., *J. Mol. Biol.*, 222:581 (1991)]. The techniques of Cole et al. and Boerner et al. are also available for the preparation of human monoclonal antibodies (Cole et al., *Monoclonal Antibodies and Cancer Therapy*, Alan R. Liss, p. 77 (1985) and Boerner et al., *J. Immunol.*, 147(1):86-95 (1991)]. Similarly, human antibodies can be made by introducing of human immunoglobulin loci into transgenic animals, e.g., mice in which the endogenous immunoglobulin genes have been partially or completely inactivated. Upon challenge, human antibody production is observed, which closely resembles that seen in humans in all respects, including gene rearrangement, assembly, and antibody repertoire. This approach is described, for example, in U.S. Patent Nos. 5,545,807; 5,545,806; 5,569,825; 5,625,126; 5,633,425; 5,661,016, and in the following scientific publications: Marks et al., *Bio/Technology* 10, 779-783 (1992); Lonberg et al., *Nature* 368 856-859 (1994);

Morrison, Nature 368, 812-13 (1994); Fishwild *et al.*, Nature Biotechnology 14, 845-51 (1996); Neuberger, Nature Biotechnology 14, 826 (1996); Lonberg and Huszar, Intern. Rev. Immunol. 13 65-93 (1995).

The antibodies may also be affinity matured using known selection and/or mutagenesis methods as described above. Preferred affinity matured antibodies have an affinity which is five times, more preferably

- 5 10 times, even more preferably 20 or 30 times greater than the starting antibody (generally murine, humanized or human) from which the matured antibody is prepared.

#### 4. Bispecific Antibodies

Bispecific antibodies are monoclonal, preferably human or humanized, antibodies that have binding specificities for at least two different antigens. In the present case, one of the binding specificities is for the PRO, the other one is for any other antigen, and preferably for a cell-surface protein or receptor or receptor subunit.

Methods for making bispecific antibodies are known in the art. Traditionally, the recombinant production of bispecific antibodies is based on the co-expression of two immunoglobulin heavy-chain/light-chain pairs, where the two heavy chains have different specificities [Milstein and Cuello, Nature, 305:537-539 (1983)]. Because of the random assortment of immunoglobulin heavy and light chains, these hybridomas (quadromas) produce a potential mixture of ten different antibody molecules, of which only one has the correct bispecific structure. The purification of the correct molecule is usually accomplished by affinity chromatography steps. Similar procedures are disclosed in WO 93/08829, published 13 May 1993, and in Traunecker *et al.*, EMBO J., 10:3655-3659 (1991).

20 Antibody variable domains with the desired binding specificities (antibody-antigen combining sites) can be fused to immunoglobulin constant domain sequences. The fusion preferably is with an immunoglobulin heavy-chain constant domain, comprising at least part of the hinge, CH2, and CH3 regions. It is preferred to have the first heavy-chain constant region (CH1) containing the site necessary for light-chain binding present in at least one of the fusions. DNAs encoding the immunoglobulin heavy-chain 25 fusions and, if desired, the immunoglobulin light chain, are inserted into separate expression vectors, and are co-transfected into a suitable host organism. For further details of generating bispecific antibodies see, for example, Suresh *et al.*, Methods in Enzymology, 121:210 (1986).

According to another approach described in WO 96/27011, the interface between a pair of antibody molecules can be engineered to maximize the percentage of heterodimers which are recovered from 30 recombinant cell culture. The preferred interface comprises at least a part of the CH3 region of an antibody constant domain. In this method, one or more small amino acid side chains from the interface of the first antibody molecule are replaced with larger side chains (e.g. tyrosine or tryptophan). Compensatory "cavities" of identical or similar size to the large side chain(s) are created on the interface of the second antibody molecule by replacing large amino acid side chains with smaller ones (e.g. alanine or threonine). 35 This provides a mechanism for increasing the yield of the heterodimer over other unwanted end-products such as homodimers.

Bispecific antibodies can be prepared as full length antibodies or antibody fragments (e.g. F(ab')<sub>2</sub> bispecific antibodies). Techniques for generating bispecific antibodies from antibody fragments have been described in the literature. For example, bispecific antibodies can be prepared can be prepared using 40 chemical linkage. Brennan *et al.*, Science 229:81 (1985) describe a procedure wherein intact antibodies are

proteolytically cleaved to generate  $F(ab')_2$  fragments. These fragments are reduced in the presence of the dithiol complexing agent sodium arsenite to stabilize vicinal dithiols and prevent intermolecular disulfide formation. The Fab' fragments generated are then converted to thionitrobenzoate (TNB) derivatives. One of the Fab'-TNB derivatives is then reconverted to the Fab'-thiol by reduction with mercaptoethylamine and is 5 mixed with an equimolar amount of the other Fab'-TNB derivative to form the bispecific antibody. The bispecific antibodies produced can be used as agents for the selective immobilization of enzymes.

Fab' fragments may be directly recovered from *E. coli* and chemically coupled to form bispecific antibodies. Shalaby *et al.*, *J. Exp. Med.* 175:217-225 (1992) describe the production of a fully humanized bispecific antibody  $F(ab')_2$  molecule. Each Fab' fragment was separately secreted from *E. coli* and 10 subjected to directed chemical coupling *in vitro* to form the bispecific antibody. The bispecific antibody thus formed was able to bind to cells overexpressing the ErbB2 receptor and normal human T cells, as well as trigger the lytic activity of human cytotoxic lymphocytes against human breast tumor targets.

Various techniques for making and isolating bispecific antibody fragments directly from recombinant cell culture have also been described. For example, bispecific antibodies have been produced 15 using leucine zippers. Kostelny *et al.*, *J. Immunol.* 148(5):1547-1553 (1992). The leucine zipper peptides from the Fos and Jun proteins were linked to the Fab' portions of two different antibodies by gene fusion. The antibody homodimers were reduced at the hinge region to form monomers and then re-oxidized to form the antibody heterodimers. This method can also be utilized for the production of antibody homodimers. The "diabody" technology described by Hollinger *et al.*, *Proc. Natl. Acad. Sci. USA* 90:6444-6448 (1993) 20 has provided an alternative mechanism for making bispecific antibody fragments. The fragments comprise a heavy-chain variable domain ( $V_H$ ) connected to a light-chain variable domain ( $V_L$ ) by a linker which is too short to allow pairing between the two domains on the same chain. Accordingly, the  $V_H$  and  $V_L$  domains of one fragment are forced to pair with the complementary  $V_L$  and  $V_H$  domains of another fragment, thereby forming two antigen-binding sites. Another strategy for making bispecific antibody fragments by the use of 25 single-chain Fv (sFv) dimers has also been reported. See, Gruber *et al.*, *J. Immunol.* 152:5368 (1994). Antibodies with more than two valencies are contemplated. For example, trispecific antibodies can be prepared. Tutt *et al.*, *J. Immunol.* 147:60 (1991).

Exemplary bispecific antibodies may bind to two different epitopes on a given PRO polypeptide herein. Alternatively, an anti-PRO polypeptide arm may be combined with an arm which binds to a 30 triggering molecule on a leukocyte such as a T-cell receptor molecule (e.g. CD2, CD3, CD28, or B7), or Fc receptors for IgG (Fc $\gamma$ R), such as Fc $\gamma$ RI (CD64), Fc $\gamma$ RII (CD32) and Fc $\gamma$ RIII (CD16) so as to focus cellular defense mechanisms to the cell expressing the particular PRO polypeptide. Bispecific antibodies may also be used to localize cytotoxic agents to cells which express a particular PRO polypeptide. These antibodies possess a PRO-binding arm and an arm which binds a cytotoxic agent or a radionuclide chelator, such as 35 EOTUBE, DPTA, DOTA, or TETA. Another bispecific antibody of interest binds the PRO polypeptide and further binds tissue factor (TF).

##### 5. Heteroconjugate Antibodies

Heteroconjugate antibodies are also within the scope of the present invention. Heteroconjugate antibodies are composed of two covalently joined antibodies. Such antibodies have, for example, been 40 proposed to target immune system cells to unwanted cells [U.S. Patent No. 4,676,980], and for treatment of

HIV infection [WO 91/00360; WO 92/200373; EP 03089]. It is contemplated that the antibodies may be prepared *in vitro* using known methods in synthetic protein chemistry, including those involving crosslinking agents. For example, immunotoxins may be constructed using a disulfide exchange reaction or by forming a thioether bond. Examples of suitable reagents for this purpose include iminothiolate and 5 methyl-4-mercaptoputyrimidate and those disclosed, for example, in U.S. Patent No. 4,676,980.

#### 6. Effector Function Engineering

It may be desirable to modify the antibody of the invention with respect to effector function, so as to enhance, *e.g.*, the effectiveness of the antibody in treating cancer. For example, cysteine residue(s) may be introduced into the Fc region, thereby allowing interchain disulfide bond formation in this region. The 10 homodimeric antibody thus generated may have improved internalization capability and/or increased complement-mediated cell killing and antibody-dependent cellular cytotoxicity (ADCC). See Caron *et al.*, *J. Exp Med.*, 176: 1191-1195 (1992) and Shope, *J. Immunol.*, 148: 2918-2922 (1992). Homodimeric antibodies with enhanced anti-tumor activity may also be prepared using heterobifunctional cross-linkers as described in Wolff *et al.* *Cancer Research*, 53: 2560-2565 (1993). Alternatively, an antibody can be 15 engineered that has dual Fc regions and may thereby have enhanced complement lysis and ADCC capabilities. See Stevenson *et al.*, *Anti-Cancer Drug Design*, 3: 219-230 (1989).

#### 7. Immunoconjugates

The invention also pertains to immunoconjugates comprising an antibody conjugated to a cytotoxic agent such as a chemotherapeutic agent, toxin (*e.g.*, an enzymatically active toxin of bacterial, fungal, plant, 20 or animal origin, or fragments thereof), or a radioactive isotope (*i.e.*, a radioconjugate).

Chemotherapeutic agents useful in the generation of such immunoconjugates have been described above. Enzymatically active toxins and fragments thereof that can be used include diphtheria A chain, nonbinding active fragments of diphtheria toxin, exotoxin A chain (from *Pseudomonas aeruginosa*), ricin A chain, abrin A chain, modeccin A chain, alpha-sarcin, *Aleurites fordii* proteins, dianthin proteins, *Phytolaca americana* proteins (PAPI, PAPII, and PAP-S), momordica charantia inhibitor, curcin, crotin, sapaonaria officinalis inhibitor, gelonin, mitogellin, restrictocin, phenomycin, enomycin, and the trichothecenes. A variety of radionuclides are available for the production of radioconjugated antibodies. Examples include <sup>212</sup>Bi, <sup>131</sup>I, <sup>131</sup>In, <sup>90</sup>Y, and <sup>186</sup>Re.

Conjugates of the antibody and cytotoxic agent are made using a variety of bifunctional protein-coupling agents such as N-succinimidyl-3-(2-pyridyldithiol) propionate (SPDP), iminothiolane (IT), bifunctional derivatives of imidoesters (such as dimethyl adipimidate HCL), active esters (such as disuccinimidyl suberate), aldehydes (such as glutaraldehyde), bis-azido compounds (such as bis-(*p*-azidobenzoyl) hexanediamine), bis-diazonium derivatives (such as bis-(*p*-diazoniumbenzoyl)-ethylenediamine), diisocyanates (such as tolyene 2,6-diisocyanate), and bis-active fluorine compounds (such as 1,5-difluoro-2,4-dinitrobenzene). For example, a ricin immunotoxin can be prepared as described in Vitetta *et al.*, *Science*, 238: 1098 (1987). Carbon-14-labeled 1-isothiocyanatobenzyl-3-methyldiethylene triaminepentaacetic acid (MX-DTPA) is an exemplary chelating agent for conjugation of radionucleotide to the antibody. See WO94/11026.

In another embodiment, the antibody may be conjugated to a "receptor" (such streptavidin) for 40 utilization in tumor pretargeting wherein the antibody-receptor conjugate is administered to the patient,

followed by removal of unbound conjugate from the circulation using a clearing agent and then administration of a "ligand" (e.g., avidin) that is conjugated to a cytotoxic agent (e.g., a radionucleotide).

#### 8. Immunoliposomes

The antibodies disclosed herein may also be formulated as immunoliposomes. Liposomes containing the antibody are prepared by methods known in the art, such as described in Epstein *et al.*, Proc. Natl. Acad. Sci. USA, 82: 3688 (1985); Hwang *et al.*, Proc. Natl. Acad. Sci. USA, 77: 4030 (1980); and U.S. Pat. Nos. 4,485,045 and 4,544,545. Liposomes with enhanced circulation time are disclosed in U.S. Patent No. 5,013,556.

Particularly useful liposomes can be generated by the reverse-phase evaporation method with a lipid composition comprising phosphatidylcholine, cholesterol, and PEG-derivatized phosphatidylethanolamine (PEG-PE). Liposomes are extruded through filters of defined pore size to yield liposomes with the desired diameter. Fab' fragments of the antibody of the present invention can be conjugated to the liposomes as described in Martin *et al.*, J. Biol. Chem., 257: 286-288 (1982) via a disulfide-interchange reaction. A chemotherapeutic agent (such as Doxorubicin) is optionally contained within the liposome. See Gabizon *et al.*, J. National Cancer Inst., 81(19): 1484 (1989).

#### M. Pharmaceutical Compositions

The active PRO molecules of the invention (e.g., PRO polypeptides, anti-PRO antibodies, and/or variants of each) as well as other molecules identified by the screening assays disclosed above, can be administered for the treatment of immune related diseases, in the form of pharmaceutical compositions.

Therapeutic formulations of the active PRO molecule, preferably a polypeptide or antibody of the invention, are prepared for storage by mixing the active molecule having the desired degree of purity with optional pharmaceutically acceptable carriers, excipients or stabilizers (*Remington's Pharmaceutical Sciences* 16th edition, Osol, A. Ed. [1980]), in the form of lyophilized formulations or aqueous solutions. Acceptable carriers, excipients, or stabilizers are nontoxic to recipients at the dosages and concentrations employed, and include buffers such as phosphate, citrate, and other organic acids; antioxidants including ascorbic acid and methionine; preservatives (such as octadecyldimethylbenzyl ammonium chloride; hexamethonium chloride; benzalkonium chloride, benzethonium chloride; phenol, butyl or benzyl alcohol; alkyl parabens such as methyl or propyl paraben; catechol; resorcinol; cyclohexanol; 3-pentanol; and m-cresol); low molecular weight (less than about 10 residues) polypeptides; proteins, such as serum albumin, gelatin, or immunoglobulins; hydrophilic polymers such as polyvinylpyrrolidone; amino acids such as glycine, glutamine, asparagine, histidine, arginine, or lysine; monosaccharides, disaccharides, and other carbohydrates including glucose, mannose, or dextrans; chelating agents such as EDTA; sugars such as sucrose, mannitol, trehalose or sorbitol; salt-forming counter-ions such as sodium; metal complexes (e.g., Zn-protein complexes); and/or non-ionic surfactants such as TWEEN<sup>TM</sup>, PLURONICS<sup>TM</sup> or polyethylene glycol (PEG).

Compounds identified by the screening assays disclosed herein can be formulated in an analogous manner, using standard techniques well known in the art.

Lipofections or liposomes can also be used to deliver the PRO molecule into cells. Where antibody fragments are used, the smallest inhibitory fragment which specifically binds to the binding domain of the target protein is preferred. For example, based upon the variable region sequences of an antibody, peptide

molecules can be designed which retain the ability to bind the target protein sequence. Such peptides can be synthesized chemically and/or produced by recombinant DNA technology (see, e.g., Marasco *et al.*, *Proc. Natl. Acad. Sci. USA* 90, 7889-7893 [1993]).

5 The formulation herein may also contain more than one active compound as necessary for the particular indication being treated, preferably those with complementary activities that do not adversely affect each other. Alternatively, or in addition, the composition may comprise a cytotoxic agent, cytokine or growth inhibitory agent. Such molecules are suitably present in combination in amounts that are effective for the purpose intended.

10 The active PRO molecules may also be entrapped in microcapsules prepared, for example, by coacervation techniques or by interfacial polymerization, for example, hydroxymethylcellulose or gelatin-microcapsules and poly-(methylmethacrylate) microcapsules, respectively, in colloidal drug delivery systems (for example, liposomes, albumin microspheres, macroemulsions, nano-particles and nanocapsules) or in macroemulsions. Such techniques are disclosed in *Remington's Pharmaceutical Sciences* 16th edition, Osol, A. Ed. (1980).

15 The formulations to be used for *in vivo* administration must be sterile. This is readily accomplished by filtration through sterile filtration membranes.

Sustained-release preparations or the PRO molecules may be prepared. Suitable examples of sustained-release preparations include semipermeable matrices of solid hydrophobic polymers containing the antibody, which matrices are in the form of shaped articles, e.g., films, or microcapsules. Examples of 20 sustained-release matrices include polyesters, hydrogels (for example, poly(2-hydroxyethyl-methacrylate), or poly(vinylalcohol)), polylactides (U.S. Pat. No. 3,773,919), copolymers of L-glutamic acid and  $\gamma$ -ethyl-L-glutamate, non-degradable ethylene-vinyl acetate, degradable lactic acid-glycolic acid copolymers such as the LUPRON DEPOT<sup>TM</sup> (injectable microspheres composed of lactic acid-glycolic acid copolymer and leuprolide acetate), and poly-D-(-)-3-hydroxybutyric acid. While polymers such as ethylene-vinyl acetate 25 and lactic acid-glycolic acid enable release of molecules for over 100 days, certain hydrogels release proteins for shorter time periods. When encapsulated antibodies remain in the body for a long time, they may denature or aggregate as a result of exposure to moisture at 37°C, resulting in a loss of biological activity and possible changes in immunogenicity. Rational strategies can be devised for stabilization depending on the mechanism involved. For example, if the aggregation mechanism is discovered to be intermolecular S-S 30 bond formation through thio-disulfide interchange, stabilization may be achieved by modifying sulphydryl residues, lyophilizing from acidic solutions, controlling moisture content, using appropriate additives, and developing specific polymer matrix compositions.

#### N. Methods of Treatment

It is contemplated that the polypeptides, antibodies and other active compounds of the present 35 invention may be used to treat various immune related diseases and conditions, such as T cell mediated diseases, including those characterized by infiltration of inflammatory cells into a tissue, stimulation of T-cell proliferation, inhibition of T-cell proliferation, increased or decreased vascular permeability or the inhibition thereof.

Exemplary conditions or disorders to be treated with the polypeptides, antibodies and other 40 compounds of the invention, include, but are not limited to systemic lupus erythematosis, rheumatoid

arthritis, juvenile chronic arthritis, osteoarthritis, spondyloarthropathies, systemic sclerosis (scleroderma), idiopathic inflammatory myopathies (dermatomyositis, polymyositis), Sjögren's syndrome, systemic vasculitis, sarcoidosis, autoimmune hemolytic anemia (immune pancytopenia, paroxysmal nocturnal hemoglobinuria), autoimmune thrombocytopenia (idiopathic thrombocytopenic purpura, immune-mediated thrombocytopenia), thyroiditis (Grave's disease, Hashimoto's thyroiditis, juvenile lymphocytic thyroiditis, atrophic thyroiditis), diabetes mellitus, immune-mediated renal disease (glomerulonephritis, tubulointerstitial nephritis), demyelinating diseases of the central and peripheral nervous systems such as multiple sclerosis, idiopathic demyelinating polyneuropathy or Guillain-Barré syndrome, and chronic inflammatory demyelinating polyneuropathy, hepatobiliary diseases such as infectious hepatitis (hepatitis A, B, C, D, E and other non-hepatotropic viruses), autoimmune chronic active hepatitis, primary biliary cirrhosis, granulomatous hepatitis, and sclerosing cholangitis, inflammatory bowel disease (ulcerative colitis: Crohn's disease), gluten-sensitive enteropathy, and Whipple's disease, autoimmune or immune-mediated skin diseases including bullous skin diseases, erythema multiforme and contact dermatitis, psoriasis, allergic diseases such as asthma, allergic rhinitis, atopic dermatitis, food hypersensitivity and urticaria, immunologic diseases of the lung such as eosinophilic pneumonias, idiopathic pulmonary fibrosis and hypersensitivity pneumonitis, transplantation associated diseases including graft rejection and graft -versus-host-disease.

In systemic lupus erythematosus, the central mediator of disease is the production of auto-reactive antibodies to self proteins/tissues and the subsequent generation of immune-mediated inflammation. Antibodies either directly or indirectly mediate tissue injury. Though T lymphocytes have not been shown to be directly involved in tissue damage, T lymphocytes are required for the development of auto-reactive antibodies. The genesis of the disease is thus T lymphocyte dependent. Multiple organs and systems are affected clinically including kidney, lung, musculoskeletal system, mucocutaneous, eye, central nervous system, cardiovascular system, gastrointestinal tract, bone marrow and blood.

Rheumatoid arthritis (RA) is a chronic systemic autoimmune inflammatory disease that mainly involves the synovial membrane of multiple joints with resultant injury to the articular cartilage. The pathogenesis is T lymphocyte dependent and is associated with the production of rheumatoid factors, auto-antibodies directed against self IgG, with the resultant formation of immune complexes that attain high levels in joint fluid and blood. These complexes in the joint may induce the marked infiltrate of lymphocytes and monocytes into the synovium and subsequent marked synovial changes; the joint space/fluid if infiltrated by similar cells with the addition of numerous neutrophils. Tissues affected are primarily the joints, often in symmetrical pattern. However, extra-articular disease also occurs in two major forms. One form is the development of extra-articular lesions with ongoing progressive joint disease and typical lesions of pulmonary fibrosis, vasculitis, and cutaneous ulcers. The second form of extra-articular disease is the so called Felty's syndrome which occurs late in the RA disease course, sometimes after joint disease has become quiescent, and involves the presence of neutropenia, thrombocytopenia and splenomegaly. This can be accompanied by vasculitis in multiple organs with formations of infarcts, skin ulcers and gangrene. Patients often also develop rheumatoid nodules in the subcutis tissue overlying affected joints; the nodules late stage have necrotic centers surrounded by a mixed inflammatory cell infiltrate. Other manifestations which can occur in RA include: pericarditis, pleuritis, coronary arteritis, intestinal pneumonitis with pulmonary fibrosis, keratoconjunctivitis sicca, and rheumatoid nodules.

Juvenile chronic arthritis is a chronic idiopathic inflammatory disease which begins often at less than 16 years of age. Its phenotype has some similarities to RA; some patients which are rheumatoid factor positive are classified as juvenile rheumatoid arthritis. The disease is sub-classified into three major categories: pauciarticular, polyarticular, and systemic. The arthritis can be severe and is typically 5 destructive and leads to joint ankylosis and retarded growth. Other manifestations can include chronic anterior uveitis and systemic amyloidosis.

Spondyloarthropathies are a group of disorders with some common clinical features and the common association with the expression of HLA-B27 gene product. The disorders include: ankylosing spondylitis, Reiter's syndrome (reactive arthritis), arthritis associated with inflammatory bowel disease, 10 spondylitis associated with psoriasis, juvenile onset spondyloarthropathy and undifferentiated spondyloarthropathy. Distinguishing features include sacroileitis with or without spondylitis; inflammatory asymmetric arthritis; association with HLA-B27 (a serologically defined allele of the HLA-B locus of class I MHC); ocular inflammation, and absence of autoantibodies associated with other rheumatoid disease. The cell most implicated as key to induction of the disease is the CD8+ T lymphocyte, a cell which targets 15 antigen presented by class I MHC molecules. CD8+ T cells may react against the class I MHC allele HLA-B27 as if it were a foreign peptide expressed by MHC class I molecules. It has been hypothesized that an epitope of HLA-B27 may mimic a bacterial or other microbial antigenic epitope and thus induce a CD8+ T cells response.

Systemic sclerosis (scleroderma) has an unknown etiology. A hallmark of the disease is induration 20 of the skin; likely this is induced by an active inflammatory process. Scleroderma can be localized or systemic; vascular lesions are common and endothelial cell injury in the microvasculature is an early and important event in the development of systemic sclerosis; the vascular injury may be immune mediated. An immunologic basis is implied by the presence of mononuclear cell infiltrates in the cutaneous lesions and the presence of anti-nuclear antibodies in many patients. ICAM-1 is often upregulated on the cell surface of 25 fibroblasts in skin lesions suggesting that T cell interaction with these cells may have a role in the pathogenesis of the disease. Other organs involved include: the gastrointestinal tract: smooth muscle atrophy and fibrosis resulting in abnormal peristalsis/motility; kidney: concentric subendothelial intimal proliferation affecting small arcuate and interlobular arteries with resultant reduced renal cortical blood flow, results in proteinuria, azotemia and hypertension; skeletal muscle: atrophy, interstitial fibrosis; 30 lung: interstitial pneumonitis and interstitial fibrosis; and heart: contraction band necrosis, scarring/fibrosis.

Idiopathic inflammatory myopathies including dermatomyositis, polymyositis and others are 35 disorders of chronic muscle inflammation of unknown etiology resulting in muscle weakness. Muscle injury/inflammation is often symmetric and progressive. Autoantibodies are associated with most forms. These myositis-specific autoantibodies are directed against and inhibit the function of components, proteins and RNA's, involved in protein synthesis.

Sjögren's syndrome is due to immune-mediated inflammation and subsequent functional destruction 40 of the tear glands and salivary glands. The disease can be associated with or accompanied by inflammatory connective tissue diseases. The disease is associated with autoantibody production against Ro and La antigens, both of which are small RNA-protein complexes. Lesions result in keratoconjunctivitis sicca,

xerostomia, with other manifestations or associations including biliary cirrhosis, peripheral or sensory neuropathy, and palpable purpura.

Systemic vasculitis are diseases in which the primary lesion is inflammation and subsequent damage to blood vessels which results in ischemia/necrosis/degeneration to tissues supplied by the affected vessels and eventual end-organ dysfunction in some cases. Vasculitides can also occur as a secondary lesion or sequelae to other immune-inflammatory mediated diseases such as rheumatoid arthritis, systemic sclerosis, etc., particularly in diseases also associated with the formation of immune complexes. Diseases in the primary systemic vasculitis group include: systemic necrotizing vasculitis: polyarteritis nodosa, allergic angiitis and granulomatosis, polyangiitis; Wegener's granulomatosis; lymphomatoid granulomatosis; and giant cell arteritis. Miscellaneous vasculitides include: mucocutaneous lymph node syndrome (MLNS or Kawasaki's disease), isolated CNS vasculitis, Behet's disease, thromboangiitis obliterans (Buerger's disease) and cutaneous necrotizing venulitis. The pathogenic mechanism of most of the types of vasculitis listed is believed to be primarily due to the deposition of immunoglobulin complexes in the vessel wall and subsequent induction of an inflammatory response either via ADCC, complement activation, or both.

Sarcoidosis is a condition of unknown etiology which is characterized by the presence of epithelioid granulomas in nearly any tissue in the body; involvement of the lung is most common. The pathogenesis involves the persistence of activated macrophages and lymphoid cells at sites of the disease with subsequent chronic sequelae resultant from the release of locally and systemically active products released by these cell types.

Autoimmune hemolytic anemia including autoimmune hemolytic anemia, immune pancytopenia, and paroxysmal nocturnal hemoglobinuria is a result of production of antibodies that react with antigens expressed on the surface of red blood cells (and in some cases other blood cells including platelets as well) and is a reflection of the removal of those antibody coated cells via complement mediated lysis and/or ADCC/Fc-receptor-mediated mechanisms.

In autoimmune thrombocytopenia including thrombocytopenic purpura, and immune-mediated thrombocytopenia in other clinical settings, platelet destruction/removal occurs as a result of either antibody or complement attaching to platelets and subsequent removal by complement lysis, ADCC or FC-receptor mediated mechanisms.

Thyroiditis including Grave's disease, Hashimoto's thyroiditis, juvenile lymphocytic thyroiditis, and atrophic thyroiditis, are the result of an autoimmune response against thyroid antigens with production of antibodies that react with proteins present in and often specific for the thyroid gland. Experimental models exist including spontaneous models: rats (BUF and BB rats) and chickens (obese chicken strain); inducible models: immunization of animals with either thyroglobulin, thyroid microsomal antigen (thyroid peroxidase).

Type I diabetes mellitus or insulin-dependent diabetes is the autoimmune destruction of pancreatic islet  $\beta$  cells; this destruction is mediated by auto-antibodies and auto-reactive T cells. Antibodies to insulin or the insulin receptor can also produce the phenotype of insulin-non-responsiveness.

Immune mediated renal diseases, including glomerulonephritis and tubulointerstitial nephritis, are the result of antibody or T lymphocyte mediated injury to renal tissue either directly as a result of the production of autoreactive antibodies or T cells against renal antigens or indirectly as a result of the

deposition of antibodies and/or immune complexes in the kidney that are reactive against other, non-renal antigens. Thus other immune-mediated diseases that result in the formation of immune-complexes can also induce immune mediated renal disease as an indirect sequelae. Both direct and indirect immune mechanisms result in inflammatory response that produces/induces lesion development in renal tissues with 5 resultant organ function impairment and in some cases progression to renal failure. Both humoral and cellular immune mechanisms can be involved in the pathogenesis of lesions.

Demyelinating diseases of the central and peripheral nervous systems, including Multiple Sclerosis; idiopathic demyelinating polyneuropathy or Guillain-Barré syndrome; and Chronic Inflammatory Demyelinating Polyneuropathy, are believed to have an autoimmune basis and result in nerve demyelination 10 as a result of damage caused to oligodendrocytes or to myelin directly. In MS there is evidence to suggest that disease induction and progression is dependent on T lymphocytes. Multiple Sclerosis is a demyelinating disease that is T lymphocyte-dependent and has either a relapsing-remitting course or a chronic progressive course. The etiology is unknown; however, viral infections, genetic predisposition, environment, and autoimmunity all contribute. Lesions contain infiltrates of predominantly T lymphocyte mediated, 15 microglial cells and infiltrating macrophages; CD4+ T lymphocytes are the predominant cell type at lesions. The mechanism of oligodendrocyte cell death and subsequent demyelination is not known but is likely T lymphocyte driven.

Inflammatory and Fibrotic Lung Disease, including Eosinophilic Pneumonias; Idiopathic Pulmonary Fibrosis, and Hypersensitivity Pneumonitis may involve a disregulated immune-inflammatory 20 response. Inhibition of that response would be of therapeutic benefit.

Autoimmune or Immune-mediated Skin Disease including Bullous Skin Diseases, Erythema Multiforme, and Contact Dermatitis are mediated by auto-antibodies, the genesis of which is T lymphocyte-dependent.

Psoriasis is a T lymphocyte-mediated inflammatory disease. Lesions contain infiltrates of T 25 lymphocytes, macrophages and antigen processing cells, and some neutrophils.

Allergic diseases, including asthma; allergic rhinitis; atopic dermatitis; food hypersensitivity; and urticaria are T lymphocyte dependent. These diseases are predominantly mediated by T lymphocyte induced inflammation, IgE mediated-inflammation or a combination of both.

Transplantation associated diseases, including Graft rejection and Graft-Versus-Host-Disease 30 (GVHD) are T lymphocyte-dependent; inhibition of T lymphocyte function is ameliorative.

Other diseases in which intervention of the immune and/or inflammatory response have benefit are infectious disease including but not limited to viral infection (including but not limited to AIDS, hepatitis A, B, C, D, E and herpes) bacterial infection, fungal infections, and protozoal and parasitic infections (molecules (or derivatives/agonists) which stimulate the MLR can be utilized therapeutically to enhance the 35 immune response to infectious agents), diseases of immunodeficiency (molecules/derivatives/agonists) which stimulate the MLR can be utilized therapeutically to enhance the immune response for conditions of inherited, acquired, infectious induced (as in HIV infection), or iatrogenic (*i.e.*, as from chemotherapy) immunodeficiency, and neoplasia.

It has been demonstrated that some human cancer patients develop an antibody and/or T 40 lymphocyte response to antigens on neoplastic cells. It has also been shown in animal models of neoplasia

that enhancement of the immune response can result in rejection or regression of that particular neoplasm. Molecules that enhance the T lymphocyte response in the MLR have utility *in vivo* in enhancing the immune response against neoplasia. Molecules which enhance the T lymphocyte proliferative response in the MLR (or small molecule agonists or antibodies that affected the same receptor in an agonistic fashion) can be used 5 therapeutically to treat cancer. Molecules that inhibit the lymphocyte response in the MLR also function *in vivo* during neoplasia to suppress the immune response to a neoplasm; such molecules can either be expressed by the neoplastic cells themselves or their expression can be induced by the neoplasm in other cells. Antagonism of such inhibitory molecules (either with antibody, small molecule antagonists or other means) enhances immune-mediated tumor rejection.

10 Additionally, inhibition of molecules with proinflammatory properties may have therapeutic benefit in reperfusion injury; stroke; myocardial infarction; atherosclerosis; acute lung injury; hemorrhagic shock; burn; sepsis/septic shock; acute tubular necrosis; endometriosis; degenerative joint disease and pancreatitis.

15 The compounds of the present invention, e.g., polypeptides or antibodies, are administered to a mammal, preferably a human, in accord with known methods, such as intravenous administration as a bolus or by continuous infusion over a period of time, by intramuscular, intraperitoneal, intracerebrospinal, 20 subcutaneous, intra-articular, intrasynovial, intrathecal, oral, topical, or inhalation (intranasal, intrapulmonary) routes. Intravenous or inhaled administration of polypeptides and antibodies is preferred.

25 In immunoadjuvant therapy, other therapeutic regimens, such administration of an anti-cancer agent, may be combined with the administration of the proteins, antibodies or compounds of the instant invention. For example, the patient to be treated with the immunoadjuvant of the invention may also receive an anti-cancer agent (chemotherapeutic agent) or radiation therapy. Preparation and dosing schedules for such chemotherapeutic agents may be used according to manufacturers' instructions or as determined empirically by the skilled practitioner. Preparation and dosing schedules for such chemotherapy are also described in *Chemotherapy Service* Ed., M.C. Perry, Williams & Wilkins, Baltimore, MD (1992). The chemotherapeutic agent may precede, or follow administration of the immunoadjuvant or may be given simultaneously therewith. Additionally, an anti-estrogen compound such as tamoxifen or an anti-progesterone such as onapristone (see, EP 616812) may be given in dosages known for such molecules.

30 It may be desirable to also administer antibodies against other immune disease associated or tumor associated antigens, such as antibodies which bind to CD20, CD11a, CD18, ErbB2, EGFR, ErbB3, ErbB4, or vascular endothelial factor (VEGF). Alternatively, or in addition, two or more antibodies binding the same or two or more different antigens disclosed herein may be coadministered to the patient. Sometimes, it 35 may be beneficial to also administer one or more cytokines to the patient. In one embodiment, the PRO polypeptides are coadministered with a growth inhibitory agent. For example, the growth inhibitory agent may be administered first, followed by a PRO polypeptide. However, simultaneous administration or administration first is also contemplated. Suitable dosages for the growth inhibitory agent are those presently used and may be lowered due to the combined action (synergy) of the growth inhibitory agent and the PRO polypeptide.

40 For the treatment or reduction in the severity of immune related disease, the appropriate dosage of an a compound of the invention will depend on the type of disease to be treated, as defined above, the severity and course of the disease, whether the agent is administered for preventive or therapeutic purposes,

previous therapy, the patient's clinical history and response to the compound, and the discretion of the attending physician. The compound is suitably administered to the patient at one time or over a series of treatments.

For example, depending on the type and severity of the disease, about 1 µg/kg to 15 mg/kg (e.g., 5 0.1-20 mg/kg) of polypeptide or antibody is an initial candidate dosage for administration to the patient, whether, for example, by one or more separate administrations, or by continuous infusion. A typical daily dosage might range from about 1 µg/kg to 100 mg/kg or more, depending on the factors mentioned above. For repeated administrations over several days or longer, depending on the condition, the treatment is sustained until a desired suppression of disease symptoms occurs. However, other dosage regimens may be 10 useful. The progress of this therapy is easily monitored by conventional techniques and assays.

15 O. Articles of Manufacture

In another embodiment of the invention, an article of manufacture containing materials (e.g., comprising a PRO molecule) useful for the diagnosis or treatment of the disorders described above is provided. The article of manufacture comprises a container and an instruction. Suitable containers include, 20 for example, bottles, vials, syringes, and test tubes. The containers may be formed from a variety of materials such as glass or plastic. The container holds a composition which is effective for diagnosing or treating the condition and may have a sterile access port (for example the container may be an intravenous solution bag or a vial having a stopper pierceable by a hypodermic injection needle). The active agent in the composition is usually a polypeptide or an antibody of the invention. An instruction or label on, or associated with, the container indicates that the composition is used for diagnosing or treating the condition of choice. The article of manufacture may further comprise a second container comprising a pharmaceutically-acceptable buffer, such as phosphate-buffered saline, Ringer's solution and dextrose solution. It may further include other materials desirable from a commercial and user standpoint, including other buffers, diluents, filters, needles, syringes, and package inserts with instructions for use.

25 P. Diagnosis and Prognosis of Immune Related Disease

Cell surface proteins, such as proteins which are overexpressed in certain immune related diseases, are excellent targets for drug candidates or disease treatment. The same proteins along with secreted proteins encoded by the genes amplified in immune related disease states find additional use in the diagnosis and prognosis of these diseases. For example, antibodies directed against the protein products of genes 30 amplified in multiple sclerosis, rheumatoid arthritis, or another immune related disease, can be used as diagnostics or prognostics.

For example, antibodies, including antibody fragments, can be used to qualitatively or quantitatively detect the expression of proteins encoded by amplified or overexpressed genes ("marker gene products"). The antibody preferably is equipped with a detectable, e.g., fluorescent label, and binding can be 35 monitored by light microscopy, flow cytometry, fluorimetry, or other techniques known in the art. These techniques are particularly suitable, if the overexpressed gene encodes a cell surface protein. Such binding assays are performed essentially as described above.

*In situ* detection of antibody binding to the marker gene products can be performed, for example, by immunofluorescence or immunoelectron microscopy. For this purpose, a histological specimen is removed 40 from the patient, and a labeled antibody is applied to it, preferably by overlaying the antibody on a biological

sample. This procedure also allows for determining the distribution of the marker gene product in the tissue examined. It will be apparent for those skilled in the art that a wide variety of histological methods are readily available for *in situ* detection.

The following examples are offered for illustrative purposes only, and are not intended to limit the scope of the present invention in any way.

All patent and literature references cited in the present specification are hereby incorporated by reference in their entirety.

#### EXAMPLES

Commercially available reagents referred to in the examples were used according to manufacturer's instructions unless otherwise indicated. The source of those cells identified in the following examples, and throughout the specification, by ATCC accession numbers is the American Type Culture Collection, Manassas, VA.

##### EXAMPLE 1: Microarray analysis of stimulated T-cells

Nucleic acid microarrays, often containing thousands of gene sequences, are useful for identifying differentially expressed genes in diseased tissues as compared to their normal counterparts. Using nucleic acid microarrays, test and control mRNA samples from test and control tissue samples are reverse transcribed and labeled to generate cDNA probes. The cDNA probes are then hybridized to an array of nucleic acids immobilized on a solid support. The array is configured such that the sequence and position of each member of the array is known. For example, a selection of genes known to be expressed in certain disease states may be arrayed on a solid support. Hybridization of a labeled probe with a particular array member indicates that the sample from which the probe was derived expresses that gene. If the hybridization signal of a probe from a test (for example, activated CD4+ T cells) sample is greater than hybridization signal of a probe from a control (for example, non-stimulated CD4 + T cells) sample, the gene or genes overexpressed in the test tissue are identified. The implication of this result is that an overexpressed protein in a test tissue is useful not only as a diagnostic marker for the presence of a disease condition, but also as a therapeutic target for treatment of a disease condition.

The methodology of hybridization of nucleic acids and microarray technology is well known in the art. In one example, the specific preparation of nucleic acids for hybridization and probes, slides, and hybridization conditions are all detailed in PCT Patent Application Serial No. PCT/US01/10482, filed on March 30, 2001 and which is herein incorporated by reference.

When CD4+ T cells mature from thymus and enter into the peripheral lymph system, they usually maintain their naive phenotype before encountering antigens specific for their T cell receptor [Sprent et al., *Annu Rev Immunol.* (2002); 20:551-79]. The binding to specific antigens presented by APC, causes T cell activation. Depending on the environment and cytokine stimulation, CD4+ T cells differentiate into a Th1 or Th2 phenotype and become effector or memory cells [Sprent et al., *Annu Rev Immunol.* (2002); 20:551-79 and Murphy et al., *Nat Rev Immunol.* (2002) Dec;2(12):933-44]. This process is known as primary activation. Having undergone primary activation, CD4+ T cells become effector or memory cells, they maintain their phenotype as Th1 or Th2. Once these cells encounter antigen again, they undergo secondary activation, but this time the response to antigen will be quicker than the primary activation and results in the

production of effector cytokines as determined by the primary activation [Sprent et al., *Annu Rev Immunol.* (2002); 20:551-79 and Murphy et al., *Annu Rev Immunol.* 2000;18:451-94].

Studies have found during the primary and secondary activation of CD4 + T cells the expression of certain genes is variable [Rogge et al., *Nature Genetics.* 25, 96 - 101 (2000) and Ouyang et al., *Proc Natl Acad Sci U S A.* (1999) Mar 30;96(7):3888-93]. The present study represents a model to identify differentially expressed genes during the primary and secondary activation response *in vitro*.

For primary activation conditions, naïve T cells were activated by anti-CD3, anti-CD28 and specific cytokines (experimental conditions are described below). This primary activation was termed condition (a). RNA isolated from cells in this condition can provide information about what genes are differentially regulated during the primary activation, and what cytokines affect gene expression during Th1 and Th2 development. After primary activation, the CD4+ T cells were maintained in culture for a week. However, as the previous activation and cytokine treatment has been imprinted into these cells and they have become either effector or memory cells. During this period, because there are no APCs or antigens, the CD4+ T cells enter a resting stage. This resting stage, termed condition (b) (with experimental conditions described below), provides information about the differences between naive vs. memory cells, and resting memory Th1 vs. resting memory Th2 cells. The resting memory Th1 and Th2 cells then undergo secondary activation under condition (c) and condition (d), with both conditions being described below. These conditions provide information about the differences between activated naive and activated memory T cells, and the differences between activated memory Th1 vs. activated memory Th2 cells. This study demonstrates differential gene expression during different stages of CD4 T cell activation and differentiation. As we know, many autoimmune diseases are caused by memory Th1 and Th2 cells. The data now provide us opportunity to find markers to identify these cells and specifically target these cells as a new therapeutic approach.

In this experiment, CD4+ T cells were purified from a single donor using the RosetteSep™ protocol (Stem Cell Technologies, Vancouver BC) which contains anti-CD8, anti-CD16, anti-CD19, anti-CD36 and anti-CD56 antibodies used to produce a population of isolated CD4 + T cells with the modification to the protocol of using 1.3 ml reagent/25ml blood. The isolated CD4+ T cells were washed by PBS (0.5% BSA) twice and counted. Naïve CD4+ T cells were further isolated by Miltenyi CD45RO beads (Miltenyi Biotec) through the autoMACSTM depletion program and the purity of the cells was determined by FACS analysis. Experiments proceeded only with >90% cell pure CD4+ T cells. At this point RNA was extracted from 50 x 10^6 CD4+ T cells for use as a baseline control. The remainder of the cells were stimulated by plate bound anti-CD3 and anti-CD28 at 20 x 10^6 cells / 6 ml T cell media / well of a 6 well plate.

On Day 1, to induce Th1 differentiation, IL-12 (1 ng/ml) and anti-IL-4 (1μ/ml) were added. For Th2 differentiation, IL-4 (5 ng/ml), anti-IL-12 (0.5 μg/ml), and anti-IFN-γ were added. For Th0 cells, anti-IL-12 (0.5 μg/ml), anti-IL-4 (1μg/ml) and anti -IFN-gamma (0.1 μg/ml) were added. All reagents were from R&D Systems (R & D Systems Inc. Minneapolis, MN).

On Day 2, cells from one well per condition were harvested for RNA purification to obtain a 48hr time point (condition (a)). On Day 3, the cells were expanded 4 fold by removing the media used for differentiation, and adding fresh media plus IL-2 and cultured for 4 days. On Day 7, the cells were washed

and counted, and the cytokine profiles were examined by intracellular cytokine staining and ELISA to determine if differentiation was complete. Half of the cells were harvested and RNA purified to determine the expression of genes in the resting state (condition (b)). IL-4 and IFN-gamma producing cells were enriched for by using the Miltenyi™ cytokine assay kit. The isolated IL-4 or IFN-gamma producing cells 5 were expanded for two more weeks by using similar conditions as above.

On Day 21, cells were harvested and subject to intracellular cytokine staining and ELISA for cytokine production analysis. The remainder of the cells were re-stimulated by anti-CD3 and anti-CD28 (secondary activation). Cells were harvested at 12 hr (condition (c)) and 48 hr (condition (d)) for RNA 10 purification. From the different conditions, RNA was extracted and analysis run on Affimax (Affymetrix Inc. Santa Clara, CA) microarray chips. Non-stimulated cells harvested immediately after purification, were subjected to the same analysis. Genes were compared whose expression was upregulated or downregulated at the different activated conditions vs. resting cells.

Below are the results of these experiments, demonstrating that various PRO polypeptides of the present invention are significantly upregulated or downregulated in isolated stimulated CD4+ T helper cells 15 as compared to unstimulated CD4+ T helper cells or isolated resting CD4+ T helper cells. As Th1 and Th2 cells play a role in normal immune defense during infection, and play a role in immune disorders, this data demonstrate that the PRO polypeptides of the present invention are useful not only as diagnostic markers for the presence of one or more immune disorders, but also serve as therapeutic targets for the treatment of those immune disorders.

SEQ ID NOs 1-6464 show nucleic acids and their encoded proteins show differential expression at 20 (condition (c)) or (condition (d)) vs. unstimulated cells as a normal control, cells that have undergone primary activation, or primary activated cells that had been in resting for 7 days. SEQ ID NO:2955, SEQ ID NO:2855, SEQ ID NO:3487, SEQ ID NO:3088, SEQ ID NO:1319, SEQ ID NO:1629, SEQ ID NO:1733, SEQ ID NO:1561, and SEQ ID NO:1699 are highly overexpressed at (condtion (c)) or (condition (d)) vs. 25 unstimulated cells as a normal control , cells that have undergone primary activation, or primary activated cells that had been in resting for 7 days.

#### EXAMPLE 2: Use of PRO as a hybridization probe

The following method describes use of a nucleotide sequence encoding PRO as a hybridization 30 probe.

DNA comprising the coding sequence of full-length or mature PRO as disclosed herein is employed as a probe to screen for homologous DNAs (such as those encoding naturally-occurring variants of PRO) in human tissue cDNA libraries or human tissue genomic libraries.

Hybridization and washing of filters containing either library DNAs is performed under the 35 following high stringency conditions. Hybridization of radiolabeled PRO-derived probe to the filters is performed in a solution of 50% formamide, 5x SSC, 0.1% SDS, 0.1% sodium pyrophosphate, 50 mM sodium phosphate, pH 6.8, 2x Denhardt's solution, and 10% dextran sulfate at 42°C for 20 hours. Washing of the filters is performed in an aqueous solution of 0.1x SSC and 0.1% SDS at 42°C.

DNA having a desired sequence identity with the DNA encoding full-length native sequence PRO 40 can then be identified using standard techniques known in the art.

EXAMPLE 3: Expression of PRO in *E. coli*

This example illustrates preparation of an unglycosylated form of PRO by recombinant expression in *E. coli*.

5       The DNA sequence encoding PRO is initially amplified using selected PCR primers. The primers should contain restriction enzyme sites which correspond to the restriction enzyme sites on the selected expression vector. A variety of expression vectors may be employed. An example of a suitable vector is pBR322 (derived from *E. coli*; see Bolivar et al., *Gene*, 2:95 (1977)) which contains genes for ampicillin and tetracycline resistance. The vector is digested with restriction enzyme and dephosphorylated. The PCR  
10      amplified sequences are then ligated into the vector. The vector will preferably include sequences which encode for an antibiotic resistance gene, a trp promoter, a polyhis leader (including the first six STII codons, polyhis sequence, and enterokinase cleavage site), the PRO coding region, lambda transcriptional terminator, and an argU gene.

15       The ligation mixture is then used to transform a selected *E. coli* strain using the methods described in Sambrook et al., *supra*. Transformants are identified by their ability to grow on LB plates and antibiotic resistant colonies are then selected. Plasmid DNA can be isolated and confirmed by restriction analysis and DNA sequencing.

20       Selected clones can be grown overnight in liquid culture medium such as LB broth supplemented with antibiotics. The overnight culture may subsequently be used to inoculate a larger scale culture. The cells are then grown to a desired optical density, during which the expression promoter is turned on.

After culturing the cells for several more hours, the cells can be harvested by centrifugation. The cell pellet obtained by the centrifugation can be solubilized using various agents known in the art, and the solubilized PRO protein can then be purified using a metal chelating column under conditions that allow tight binding of the protein.

25       PRO may be expressed in *E. coli* in a poly-His tagged form, using the following procedure. The DNA encoding PRO is initially amplified using selected PCR primers. The primers will contain restriction enzyme sites which correspond to the restriction enzyme sites on the selected expression vector, and other useful sequences providing for efficient and reliable translation initiation, rapid purification on a metal chelation column, and proteolytic removal with enterokinase. The PCR-amplified, poly-His tagged  
30      sequences are then ligated into an expression vector, which is used to transform an *E. coli* host based on strain 52 (W3110 fuhA(tonA) lon galE rpoHts(htpRts) clpP(lacIq)). Transformants are first grown in LB containing 50 mg/ml carbenicillin at 30°C with shaking until an O.D.600 of 3-5 is reached. Cultures are then diluted 50-100 fold into CRAP media (prepared by mixing 3.57 g (NH<sub>4</sub>)<sub>2</sub>SO<sub>4</sub>, 0.71 g sodium citrate•2H<sub>2</sub>O, 1.07 g KCl, 5.36 g Difco yeast extract, 5.36 g Sheffield hycase SF in 500 mL water, as well as  
35      110 mM MPOS, pH 7.3, 0.55% (w/v) glucose and 7 mM MgSO<sub>4</sub>) and grown for approximately 20-30 hours at 30°C with shaking. Samples are removed to verify expression by SDS-PAGE analysis, and the bulk culture is centrifuged to pellet the cells. Cell pellets are frozen until purification and refolding.

40       *E. coli* paste from 0.5 to 1 L fermentations (6-10 g pellets) is resuspended in 10 volumes (w/v) in 7 M guanidine, 20 mM Tris, pH 8 buffer. Solid sodium sulfite and sodium tetrathionate is added to make final concentrations of 0.1M and 0.02 M, respectively, and the solution is stirred overnight at 4°C. This step

results in a denatured protein with all cysteine residues blocked by sulfitolization. The solution is centrifuged at 40,000 rpm in a Beckman Ultracentrifuge for 30 min. The supernatant is diluted with 3-5 volumes of metal chelate column buffer (6 M guanidine, 20 mM Tris, pH 7.4) and filtered through 0.22 micron filters to clarify. The clarified extract is loaded onto a 5 ml Qiagen Ni-NTA metal chelate column equilibrated in the metal chelate column buffer. The column is washed with additional buffer containing 50 mM imidazole (Calbiochem, Utrol grade), pH 7.4. The protein is eluted with buffer containing 250 mM imidazole. Fractions containing the desired protein are pooled and stored at 4°C. Protein concentration is estimated by its absorbance at 280 nm using the calculated extinction coefficient based on its amino acid sequence.

The proteins are refolded by diluting the sample slowly into freshly prepared refolding buffer consisting of: 20 mM Tris, pH 8.6, 0.3 M NaCl, 2.5 M urea, 5 mM cysteine, 20 mM glycine and 1 mM EDTA. Refolding volumes are chosen so that the final protein concentration is between 50 to 100 micrograms/ml. The refolding solution is stirred gently at 4°C for 12-36 hours. The refolding reaction is quenched by the addition of TFA to a final concentration of 0.4% (pH of approximately 3). Before further purification of the protein, the solution is filtered through a 0.22 micron filter and acetonitrile is added to 2-10% final concentration. The refolded protein is chromatographed on a Poros R1/H reversed phase column using a mobile buffer of 0.1% TFA with elution with a gradient of acetonitrile from 10 to 80%. Aliquots of fractions with A280 absorbance are analyzed on SDS polyacrylamide gels and fractions containing homogeneous refolded protein are pooled. Generally, the properly refolded species of most proteins are eluted at the lowest concentrations of acetonitrile since those species are the most compact with their hydrophobic interiors shielded from interaction with the reversed phase resin. Aggregated species are usually eluted at higher acetonitrile concentrations. In addition to resolving misfolded forms of proteins from the desired form, the reversed phase step also removes endotoxin from the samples.

Fractions containing the desired folded PRO polypeptide are pooled and the acetonitrile removed using a gentle stream of nitrogen directed at the solution. Proteins are formulated into 20 mM Hepes, pH 6.8 with 0.14 M sodium chloride and 4% mannitol by dialysis or by gel filtration using G25 Superfine (Pharmacia) resins equilibrated in the formulation buffer and sterile filtered.

Many of the PRO polypeptides disclosed herein were successfully expressed as described above.

#### EXAMPLE 4: Expression of PRO in mammalian cells

This example illustrates preparation of a potentially glycosylated form of PRO by recombinant expression in mammalian cells.

The vector, pRK5 (see EP 307,247, published March 15, 1989), is employed as the expression vector. Optionally, the PRO DNA is ligated into pRK5 with selected restriction enzymes to allow insertion of the PRO DNA using ligation methods such as described in Sambrook et al., *supra*. The resulting vector is called pRK5-PRO.

In one embodiment, the selected host cells may be 293 cells. Human 293 cells (ATCC CCL 1573) are grown to confluence in tissue culture plates in medium such as DMEM supplemented with fetal calf serum and optionally, nutrient components and/or antibiotics. About 10 µg pRK5-PRO DNA is mixed with about 1 µg DNA encoding the VA RNA gene [Thimmappaya et al., *Cell*, 31:543 (1982)] and dissolved in 40 500 µl of 1 mM Tris-HCl, 0.1 mM EDTA, 0.227 M CaCl<sub>2</sub>. To this mixture is added, dropwise, 500 µl of 50

mM HEPES (pH 7.35), 280 mM NaCl, 1.5 mM NaPO<sub>4</sub>, and a precipitate is allowed to form for 10 minutes at 25°C. The precipitate is suspended and added to the 293 cells and allowed to settle for about four hours at 37°C. The culture medium is aspirated off and 2 ml of 20% glycerol in PBS is added for 30 seconds. The 293 cells are then washed with serum free medium, fresh medium is added and the cells are incubated for 5 about 5 days.

Approximately 24 hours after the transfections, the culture medium is removed and replaced with culture medium (alone) or culture medium containing 200 µCi/ml <sup>35</sup>S-cysteine and 200 µCi/ml <sup>35</sup>S-methionine. After a 12 hour incubation, the conditioned medium is collected, concentrated on a spin filter, and loaded onto a 15% SDS gel. The processed gel may be dried and exposed to film for a selected period 10 of time to reveal the presence of PRO polypeptide. The cultures containing transfected cells may undergo further incubation (in serum free medium) and the medium is tested in selected bioassays.

In an alternative technique, PRO may be introduced into 293 cells transiently using the dextran sulfate method described by Somparyrac et al., Proc. Natl. Acad. Sci., 75:7575 (1981). 293 cells are grown to maximal density in a spinner flask and 700 µg pRK5-PRO DNA is added. The cells are first concentrated 15 from the spinner flask by centrifugation and washed with PBS. The DNA-dextran precipitate is incubated on the cell pellet for four hours. The cells are treated with 20% glycerol for 90 seconds, washed with tissue culture medium, and re-introduced into the spinner flask containing tissue culture medium, 5 µg/ml bovine insulin and 0.1 µg/ml bovine transferrin. After about four days, the conditioned media is centrifuged and filtered to remove cells and debris. The sample containing expressed PRO can then be concentrated and 20 purified by any selected method, such as dialysis and/or column chromatography.

In another embodiment, PRO can be expressed in CHO cells. The pRK5-PRO can be transfected into CHO cells using known reagents such as CaPO<sub>4</sub> or DEAE-dextran. As described above, the cell cultures can be incubated, and the medium replaced with culture medium (alone) or medium containing a radiolabel such as <sup>35</sup>S-methionine. After determining the presence of PRO polypeptide, the culture medium 25 may be replaced with serum free medium. Preferably, the cultures are incubated for about 6 days, and then the conditioned medium is harvested. The medium containing the expressed PRO can then be concentrated and purified by any selected method.

Epitope-tagged PRO may also be expressed in host CHO cells. The PRO may be subcloned out of the pRK5 vector. The subclone insert can undergo PCR to fuse in frame with a selected epitope tag such as 30 a poly-his tag into a Baculovirus expression vector. The poly-his tagged PRO insert can then be subcloned into a SV40 promoter/enhancer containing vector containing a selection marker such as DHFR for selection of stable clones. Finally, the CHO cells can be transfected (as described above) with the SV40 promoter/enhancer containing vector. Labeling may be performed, as described above, to verify expression. The culture medium containing the expressed poly-His tagged PRO can then be concentrated and purified 35 by any selected method, such as by Ni<sup>2+</sup>-chelate affinity chromatography.

PRO may also be expressed in CHO and/or COS cells by a transient expression procedure or in CHO cells by another stable expression procedure.

Stable expression in CHO cells is performed using the following procedure. The proteins are expressed as an IgG construct (immunoadhesin), in which the coding sequences for the soluble forms (e.g.

extracellular domains) of the respective proteins are fused to an IgG1 constant region sequence containing the hinge, CH2 and CH2 domains and/or is a poly-His tagged form.

Following PCR amplification, the respective DNAs are subcloned in a CHO expression vector using standard techniques as described in Ausubel et al., Current Protocols of Molecular Biology, Unit 3.16, John Wiley and Sons (1997). CHO expression vectors are constructed to have compatible restriction sites 5' and 3' of the DNA of interest to allow the convenient shuttling of cDNA's. The vector used expression in CHO cells is as described in Lucas et al., Nucl. Acids Res. 24:9 (1774-1779 (1996), and uses the SV40 early promoter/enhancer to drive expression of the cDNA of interest and dihydrofolate reductase (DHFR). DHFR expression permits selection for stable maintenance of the plasmid following transfection.

10       Twelve micrograms of the desired plasmid DNA is introduced into approximately 10 million CHO cells using commercially available transfection reagents Superfect® (Qiagen), Dospex® or Fugene® (Boehringer Mannheim). The cells are grown as described in Lucas et al., supra. Approximately  $3 \times 10^7$  cells are frozen in an ampule for further growth and production as described below.

15       The ampules containing the plasmid DNA are thawed by placement into water bath and mixed by vortexing. The contents are pipetted into a centrifuge tube containing 10 mL of media and centrifuged at 1000 rpm for 5 minutes. The supernatant is aspirated and the cells are resuspended in 10 mL of selective media (0.2 µm filtered PS20 with 5% 0.2 µm diafiltered fetal bovine serum). The cells are then aliquoted into a 100 mL spinner containing 90 mL of selective media. After 1-2 days, the cells are transferred into a 250 mL spinner filled with 150 mL selective growth medium and incubated at 37°C. After another 2-3 days, 20       250 mL, 500 mL and 2000 mL spinners are seeded with  $3 \times 10^5$  cells/mL. The cell media is exchanged with fresh media by centrifugation and resuspension in production medium. Although any suitable CHO media may be employed, a production medium described in U.S. Patent No. 5,122,469, issued June 16, 1992 may actually be used. A 3L production spinner is seeded at  $1.2 \times 10^6$  cells/mL. On day 0, pH is determined. On day 1, the spinner is sampled and sparging with filtered air is commenced. On day 2, the spinner is sampled, 25       the temperature shifted to 33°C, and 30 mL of 500 g/L glucose and 0.6 mL of 10% antifoam (e.g., 35% polydimethylsiloxane emulsion, Dow Corning 365 Medical Grade Emulsion) taken. Throughout the production, the pH is adjusted as necessary to keep it at around 7.2. After 10 days, or until the viability dropped below 70%, the cell culture is harvested by centrifugation and filtering through a 0.22 µm filter. The filtrate was either stored at 4°C or immediately loaded onto columns for purification.

30       For the poly-His tagged constructs, the proteins are purified using a Ni-NTA column (Qiagen). Before purification, imidazole is added to the conditioned media to a concentration of 5 mM. The conditioned media is pumped onto a 6 ml Ni-NTA column equilibrated in 20 mM Hepes, pH 7.4, buffer containing 0.3 M NaCl and 5 mM imidazole at a flow rate of 4-5 ml/min. at 4°C. After loading, the column is washed with additional equilibration buffer and the protein eluted with equilibration buffer containing 0.25 M imidazole. The highly purified protein is subsequently desalting into a storage buffer containing 10 mM Hepes, 0.14 M NaCl and 4% mannitol, pH 6.8, with a 25 ml G25 Superfine (Pharmacia) column and stored at -80°C.

35       Immunoadhesin (Fc-containing) constructs are purified from the conditioned media as follows. The conditioned medium is pumped onto a 5 ml Protein A column (Pharmacia) which had been equilibrated in 20 mM Na phosphate buffer, pH 6.8. After loading, the column is washed extensively with equilibration

buffer before elution with 100 mM citric acid, pH 3.5. The eluted protein is immediately neutralized by collecting 1 ml fractions into tubes containing 275 µl of 1 M Tris buffer, pH 9. The highly purified protein is subsequently desalting into storage buffer as described above for the poly-His tagged proteins. The homogeneity is assessed by SDS polyacrylamide gels and by N-terminal amino acid sequencing by Edman degradation.

Many of the PRO polypeptides disclosed herein were successfully expressed as described above.

**EXAMPLE 5: Expression of PRO in Yeast**

The following method describes recombinant expression of PRO in yeast.

First, yeast expression vectors are constructed for intracellular production or secretion of PRO from the ADH2/GAPDH promoter. DNA encoding PRO and the promoter is inserted into suitable restriction enzyme sites in the selected plasmid to direct intracellular expression of PRO. For secretion, DNA encoding PRO can be cloned into the selected plasmid, together with DNA encoding the ADH2/GAPDH promoter, a native PRO signal peptide or other mammalian signal peptide, or, for example, a yeast alpha-factor or invertase secretory signal/leader sequence, and linker sequences (if needed) for expression of PRO.

Yeast cells, such as yeast strain AB110, can then be transformed with the expression plasmids described above and cultured in selected fermentation media. The transformed yeast supernatants can be analyzed by precipitation with 10% trichloroacetic acid and separation by SDS-PAGE, followed by staining of the gels with Coomassie Blue stain.

Recombinant PRO can subsequently be isolated and purified by removing the yeast cells from the fermentation medium by centrifugation and then concentrating the medium using selected cartridge filters. The concentrate containing PRO may further be purified using selected column chromatography resins.

Many of the PRO polypeptides disclosed herein were successfully expressed as described above.

**EXAMPLE 6: Expression of PRO in Baculovirus-Infected Insect Cells**

The following method describes recombinant expression of PRO in Baculovirus-infected insect cells.

The sequence coding for PRO is fused upstream of an epitope tag contained within a baculovirus expression vector. Such epitope tags include poly-his tags and immunoglobulin tags (like Fc regions of IgG). A variety of plasmids may be employed, including plasmids derived from commercially available plasmids such as pVL1393 (Novagen). Briefly, the sequence encoding PRO or the desired portion of the coding sequence of PRO such as the sequence encoding the extracellular domain of a transmembrane protein or the sequence encoding the mature protein if the protein is extracellular is amplified by PCR with primers complementary to the 5' and 3' regions. The 5' primer may incorporate flanking (selected) restriction enzyme sites. The product is then digested with those selected restriction enzymes and subcloned into the expression vector.

Recombinant baculovirus is generated by co-transfected the above plasmid and BaculoGold<sup>TM</sup> virus DNA (Pharmingen) into *Spodoptera frugiperda* ("Sf9") cells (ATCC CRL 1711) using lipofectin (commercially available from GIBCO-BRL). After 4 - 5 days of incubation at 28°C, the released viruses are harvested and used for further amplifications. Viral infection and protein expression are performed as

described by O'Reilley et al., *Baculovirus expression vectors: A Laboratory Manual*, Oxford: Oxford University Press (1994).

Expressed poly-his tagged PRO can then be purified, for example, by Ni<sup>2+</sup>-chelate affinity chromatography as follows. Extracts are prepared from recombinant virus-infected Sf9 cells as described by 5 Rupert et al., *Nature*, 362:175-179 (1993). Briefly, Sf9 cells are washed, resuspended in sonication buffer (25 mL Hepes, pH 7.9; 12.5 mM MgCl<sub>2</sub>; 0.1 mM EDTA; 10% glycerol; 0.1% NP-40; 0.4 M KCl), and sonicated twice for 20 seconds on ice. The sonicates are cleared by centrifugation, and the supernatant is diluted 50-fold in loading buffer (50 mM phosphate, 300 mM NaCl, 10% glycerol, pH 7.8) and filtered through a 0.45 µm filter. A Ni<sup>2+</sup>-NTA agarose column (commercially available from Qiagen) is prepared 10 with a bed volume of 5 mL, washed with 25 mL of water and equilibrated with 25 mL of loading buffer. The filtered cell extract is loaded onto the column at 0.5 mL per minute. The column is washed to baseline A<sub>280</sub> with loading buffer, at which point fraction collection is started. Next, the column is washed with a secondary wash buffer (50 mM phosphate; 300 mM NaCl, 10% glycerol, pH 6.0), which elutes 15 nonspecifically bound protein. After reaching A<sub>280</sub> baseline again, the column is developed with a 0 to 500 mM Imidazole gradient in the secondary wash buffer. One mL fractions are collected and analyzed by SDS-PAGE and silver staining or Western blot with Ni<sup>2+</sup>-NTA-conjugated to alkaline phosphatase (Qiagen). Fractions containing the eluted His<sub>10</sub>-tagged PRO are pooled and dialyzed against loading buffer.

Alternatively, purification of the IgG tagged (or Fc tagged) PRO can be performed using known chromatography techniques, including for instance, Protein A or protein G column chromatography.

20 Many of the PRO polypeptides disclosed herein were successfully expressed as described above.

#### EXAMPLE 7: Preparation of Antibodies that Bind PRO

This example illustrates preparation of monoclonal antibodies which can specifically bind PRO.

Techniques for producing the monoclonal antibodies are known in the art and are described, for 25 instance, in Goding, *supra*. Immunogens that may be employed include purified PRO, fusion proteins containing PRO, and cells expressing recombinant PRO on the cell surface. Selection of the immunogen can be made by the skilled artisan without undue experimentation.

Mice, such as Balb/c, are immunized with the PRO immunogen emulsified in complete Freund's adjuvant and injected subcutaneously or intraperitoneally in an amount from 1-100 micrograms.

30 Alternatively, the immunogen is emulsified in MPL-TDM adjuvant (Ribi Immunochemical Research, Hamilton, MT) and injected into the animal's hind foot pads. The immunized mice are then boosted 10 to 12 days later with additional immunogen emulsified in the selected adjuvant. Thereafter, for several weeks, the mice may also be boosted with additional immunization injections. Serum samples may be periodically obtained from the mice by retro-orbital bleeding for testing in ELISA assays to detect anti-PRO antibodies.

35 After a suitable antibody titer has been detected, the animals "positive" for antibodies can be injected with a final intravenous injection of PRO. Three to four days later, the mice are sacrificed and the spleen cells are harvested. The spleen cells are then fused (using 35% polyethylene glycol) to a selected murine myeloma cell line such as P3X63AgU.1, available from ATCC, No. CRL 1597. The fusions generate hybridoma cells which can then be plated in 96 well tissue culture plates containing HAT

(hypoxanthine, aminopterin, and thymidine) medium to inhibit proliferation of non-fused cells, myeloma hybrids, and spleen cell hybrids.

The hybridoma cells will be screened in an ELISA for reactivity against PRO. Determination of "positive" hybridoma cells secreting the desired monoclonal antibodies against PRO is within the skill in the art.

5 The positive hybridoma cells can be injected intraperitoneally into syngeneic Balb/c mice to produce ascites containing the anti-PRO monoclonal antibodies. Alternatively, the hybridoma cells can be grown in tissue culture flasks or roller bottles. Purification of the monoclonal antibodies produced in the ascites can be accomplished using ammonium sulfate precipitation, followed by gel exclusion

10 chromatography. Alternatively, affinity chromatography based upon binding of antibody to protein A or protein G can be employed.

EXAMPLE 8: Purification of PRO Polypeptides Using Specific Antibodies

Native or recombinant PRO polypeptides may be purified by a variety of standard techniques in the art of protein purification. For example, pro-PRO polypeptide, mature PRO polypeptide, or pre-PRO polypeptide is purified by immunoaffinity chromatography using antibodies specific for the PRO polypeptide of interest. In general, an immunoaffinity column is constructed by covalently coupling the anti-PRO polypeptide antibody to an activated chromatographic resin.

20 Polyclonal immunoglobulins are prepared from immune sera either by precipitation with ammonium sulfate or by purification on immobilized Protein A (Pharmacia LKB Biotechnology, Piscataway, N.J.). Likewise, monoclonal antibodies are prepared from mouse ascites fluid by ammonium sulfate precipitation or chromatography on immobilized Protein A. Partially purified immunoglobulin is covalently attached to a chromatographic resin such as CnBr-activated SEPHAROSE™ (Pharmacia LKB Biotechnology). The antibody is coupled to the resin, the resin is blocked, and the derivative resin is washed

25 according to the manufacturer's instructions.

Such an immunoaffinity column is utilized in the purification of PRO polypeptide by preparing a fraction from cells containing PRO polypeptide in a soluble form. This preparation is derived by solubilization of the whole cell or of a subcellular fraction obtained via differential centrifugation by the addition of detergent or by other methods well known in the art. Alternatively, soluble PRO polypeptide containing a signal sequence may be secreted in useful quantity into the medium in which the cells are grown.

30 A soluble PRO polypeptide-containing preparation is passed over the immunoaffinity column, and the column is washed under conditions that allow the preferential absorbance of PRO polypeptide (e.g., high ionic strength buffers in the presence of detergent). Then, the column is eluted under conditions that disrupt 35 antibody/PRO polypeptide binding (e.g., a low pH buffer such as approximately pH 2-3, or a high concentration of a chaotrope such as urea or thiocyanate ion), and PRO polypeptide is collected.

EXAMPLE 9: Drug Screening

This invention is particularly useful for screening compounds by using PRO polypeptides or 40 binding fragment thereof in any of a variety of drug screening techniques. The PRO polypeptide or

fragment employed in such a test may either be free in solution, affixed to a solid support, borne on a cell surface, or located intracellularly. One method of drug screening utilizes eukaryotic or prokaryotic host cells which are stably transformed with recombinant nucleic acids expressing the PRO polypeptide or fragment. Drugs are screened against such transformed cells in competitive binding assays. Such cells, either in viable 5 or fixed form, can be used for standard binding assays. One may measure, for example, the formation of complexes between PRO polypeptide or a fragment and the agent being tested. Alternatively, one can examine the diminution in complex formation between the PRO polypeptide and its target cell or target receptors caused by the agent being tested.

Thus, the present invention provides methods of screening for drugs or any other agents which can 10 affect a PRO polypeptide-associated disease or disorder. These methods comprise contacting such an agent with an PRO polypeptide or fragment thereof and assaying (I) for the presence of a complex between the agent and the PRO polypeptide or fragment, or (ii) for the presence of a complex between the PRO polypeptide or fragment and the cell, by methods well known in the art. In such competitive binding assays, the PRO polypeptide or fragment is typically labeled. After suitable incubation, free PRO polypeptide or 15 fragment is separated from that present in bound form, and the amount of free or uncomplexed label is a measure of the ability of the particular agent to bind to PRO polypeptide or to interfere with the PRO polypeptide/cell complex.

Another technique for drug screening provides high throughput screening for compounds having 20 suitable binding affinity to a polypeptide and is described in detail in WO 84/03564, published on September 13, 1984. Briefly stated, large numbers of different small peptide test compounds are synthesized on a solid substrate, such as plastic pins or some other surface. As applied to a PRO polypeptide, the peptide test compounds are reacted with PRO polypeptide and washed. Bound PRO polypeptide is detected by methods well known in the art. Purified PRO polypeptide can also be coated directly onto plates for use in the aforementioned drug screening techniques. In addition, non-neutralizing antibodies can be used to capture 25 the peptide and immobilize it on the solid support.

This invention also contemplates the use of competitive drug screening assays in which neutralizing 30 antibodies capable of binding PRO polypeptide specifically compete with a test compound for binding to PRO polypeptide or fragments thereof. In this manner, the antibodies can be used to detect the presence of any peptide which shares one or more antigenic determinants with PRO polypeptide.

#### EXAMPLE 10: Rational Drug Design

The goal of rational drug design is to produce structural analogs of biologically active polypeptide of interest (*i.e.*, a PRO polypeptide) or of small molecules with which they interact, *e.g.*, agonists, antagonists, or inhibitors. Any of these examples can be used to fashion drugs which are more active or 35 stable forms of the PRO polypeptide or which enhance or interfere with the function of the PRO polypeptide *in vivo* (*c.f.*, Hodgson, *Bio/Technology*, 9: 19-21 (1991)).

In one approach, the three-dimensional structure of the PRO polypeptide, or of a PRO 40 polypeptide-inhibitor complex, is determined by x-ray crystallography, by computer modeling or, most typically, by a combination of the two approaches. Both the shape and charges of the PRO polypeptide must be ascertained to elucidate the structure and to determine active site(s) of the molecule. Less often, useful

information regarding the structure of the PRO polypeptide may be gained by modeling based on the structure of homologous proteins. In both cases, relevant structural information is used to design analogous PRO polypeptide-like molecules or to identify efficient inhibitors. Useful examples of rational drug design may include molecules which have improved activity or stability as shown by Braxton and Wells,  
5 Biochemistry, 31:7796-7801 (1992) or which act as inhibitors, agonists, or antagonists of native peptides as shown by Athauda *et al.*, J. Biochem., 113:742-746 (1993).

It is also possible to isolate a target-specific antibody, selected by functional assay, as described above, and then to solve its crystal structure. This approach, in principle, yields a pharmacore upon which subsequent drug design can be based. It is possible to bypass protein crystallography altogether by  
10 generating anti-idiotypic antibodies (anti-ids) to a functional, pharmacologically active antibody. As a mirror image of a mirror image, the binding site of the anti-ids would be expected to be an analog of the original receptor. The anti-id could then be used to identify and isolate peptides from banks of chemically or biologically produced peptides. The isolated peptides would then act as the pharmacore.

By virtue of the present invention, sufficient amounts of the PRO polypeptide may be made  
15 available to perform such analytical studies as X-ray crystallography. In addition, knowledge of the PRO polypeptide amino acid sequence provided herein will provide guidance to those employing computer modeling techniques in place of or in addition to x-ray crystallography.

The foregoing written specification is considered to be sufficient to enable one skilled in the art to practice the invention. The present invention is not to be limited in scope by the construct deposited, since  
20 the deposited embodiment is intended as a single illustration of certain aspects of the invention and any constructs that are functionally equivalent are within the scope of this invention. The deposit of material herein does not constitute an admission that the written description herein contained is inadequate to enable the practice of any aspect of the invention, including the best mode thereof, nor is it to be construed as limiting the scope of the claims to the specific illustrations that it represents. Indeed, various modifications  
25 of the invention in addition to those shown and described herein will become apparent to those skilled in the art from the foregoing description and fall within the scope of the appended claims.

APPENDIX A

## List of Figures

- Figure 1: DNA344243, U25789, 200012\_x.at  
 Figure 2: PRO94991  
 Figure 3: DNA326466, NP\_004530.1, 200027\_at  
 Figure 4: PRO60800  
 Figure 5: DNA326324, NP\_000972.1, 200029\_at  
 Figure 6: PRO4738  
 Figure 7: DNA344244, NP\_006324.1, 200056\_s.at  
 Figure 8: PRO61385  
 Figure 9: DNA304680, NP\_031381.2, 200064\_at  
 Figure 10: PRO71106  
 Figure 11: DNA325222, NP\_000967.1, 200088\_x.at  
 Figure 12: PRO62236  
 Figure 13: DNA270963, NP\_003326.1, 1294\_at  
 Figure 14: PRO59293  
 Figure 15: DNA188207, NP\_005371.1, 37005\_at  
 Figure 16: PRO21719  
 Figure 17: DNA333633, NP\_055697.1, 38149\_at  
 Figure 18: PRO88275  
 Figure 19: DNA254127, NP\_008925.1, 38241\_at  
 Figure 20: PRO49242  
 Figure 21A-B: DNA329908, BAA13246.1, 38892\_at  
 Figure 22: PRO85225  
 Figure 23: DNA327523, NP\_004916.1, 39248\_at  
 Figure 24: PRO38028  
 Figure 25: DNA328357, 1452321.2, 39582\_at  
 Figure 26: PRO84217  
 Figure 27A-B: DNA273398, NP\_056383.1, 41577\_at  
 Figure 28: PRO61398  
 Figure 29: DNA327526, NP\_065727.2, 45288\_at  
 Figure 30: PRO83574  
 Figure 31: DNA344245, AF177331, 47069\_at  
 Figure 32: PRO94992  
 Figure 33A-B: DNA335121, NP\_066300.1, 47550\_at  
 Figure 34: PRO89524  
 Figure 35: DNA344246, NP\_009093.1, 50221\_at  
 Figure 36: PRO94993  
 Figure 37A-B: DNA226870, NP\_000782.1, 48808\_at  
 Figure 38: PRO37333  
 Figure 39A-B: DNA194778, NP\_055545.1, 200617\_at  
 Figure 40: PRO24056  
 Figure 41: DNA287245, NP\_004175.1, 200628\_s.at  
 Figure 42: PRO69520  
 Figure 43: DNA287245, NM\_004184, 200629\_at  
 Figure 44: PRO69520  
 Figure 45: DNA327532, NP\_002056.2, 200648\_s.at  
 Figure 46: PRO71134  
 Figure 47: DNA226063, X05130, 200656\_s.at  
 Figure 48: PRO36526  
 Figure 49: DNA274759, NP\_005611.1, 200660\_at  
 Figure 50: PRO62529  
 Figure 51: DNA324276, NP\_000985.1, 200674\_s.at  
 Figure 52: PRO80959  
 Figure 53: DNA304669, NP\_002119.1, 200679\_x.at  
 Figure 54: PRO71096  
 Figure 55A-B: DNA344247, 7684654.2, 200690\_at  
 Figure 56: PRO94994  
 Figure 57: DNA344248, NP\_004125.3, 200691\_s.at  
 Figure 58: PRO94995  
 Figure 59: DNA344249, NM\_004134, 200692\_s.at  
 Figure 60: PRO94996  
 Figure 61: DNA324897, NP\_006845.1, 200700\_s.at  
 Figure 62: PRO12468  
 Figure 63: DNA328375, NP\_002071.1, 200708\_at  
 Figure 64: PRO80880  
 Figure 65: DNA327114, NP\_006004.1, 200725\_x.at  
 Figure 66: PRO62466  
 Figure 67: DNA323943, NP\_001021.1, 200741\_s.at  
 Figure 68: PRO80676  
 Figure 69: DNA344250, NP\_000382.3, 200742\_s.at  
 Figure 70: PRO94997  
 Figure 71: DNA304659, NP\_002023.1, 200748\_s.at  
 Figure 72: PRO71086  
 Figure 73: DNA344251, 7762050.6, 200749\_at  
 Figure 74: PRO94998  
 Figure 75: DNA287207, NP\_006316.1, 200750\_s.at  
 Figure 76: PRO39268  
 Figure 77A-B: DNA344252, NP\_001377.1, 200762\_at  
 Figure 78: PRO62709  
 Figure 79: DNA225584, NP\_001145.1, 200782\_at  
 Figure 80: PRO36047  
 Figure 81: DNA226262, NP\_005554.1, 200783\_s.at  
 Figure 82: PRO36725  
 Figure 83: DNA324060, NP\_002530.1, 200790\_at  
 Figure 84: PRO80773  
 Figure 85: DNA287211, NP\_002147.1, 200806\_s.at  
 Figure 86: PRO69492  
 Figure 87: DNA287211, NM\_002156, 200807\_s.at  
 Figure 88: PRO69492  
 Figure 89: DNA325222, NM\_000976, 200809\_x.at  
 Figure 90: PRO62236  
 Figure 91: DNA269874, NP\_001271.1, 200810\_s.at  
 Figure 92: PRO58272  
 Figure 93: DNA269874, NM\_001280, 200811\_at  
 Figure 94: PRO58272  
 Figure 95: DNA227795, NP\_006420.1, 200812\_at  
 Figure 96: PRO38258  
 Figure 97: DNA189687, NP\_000843.1, 200824\_at  
 Figure 98: PRO25845  
 Figure 99A-B: DNA255281, NP\_006380.1,  
 200825\_s.at  
 Figure 100: PRO50357  
 Figure 101: DNA88165, M14221, 200838\_at  
 Figure 102: PRO2678  
 Figure 103: DNA196817, L16510, 200839\_s.at  
 Figure 104: PRO3344  
 Figure 105: DNA326615, NP\_000971.1, 200869\_at  
 Figure 106: PRO82971  
 Figure 107: DNA226112, NP\_002769.1, 200871\_s.at

- Figure 108: PRO36575  
Figure 109: DNA254537, NP\_002957.1, 200872\_at  
Figure 110: PRO49642  
Figure 111: DNA254572, NP\_006576.1, 200873\_s\_at  
Figure 112: PRO49675  
Figure 113: DNA271030, NP\_006383.1, 200875\_s\_at  
Figure 114: PRO59358  
Figure 115: DNA324107, NP\_006421.1, 200877\_at  
Figure 116: PRO80814  
Figure 117: DNA328379, BC015869, 200878\_at  
Figure 118: PRO84234  
Figure 119: DNA329099, 1164406.9, 200880\_at  
Figure 120: PRO60127  
Figure 121: DNA271847, NP\_001530.1, 200881\_s\_at  
Figure 122: PRO60127  
Figure 123: DNA226124, NP\_003135.1, 200890\_s\_at  
Figure 124: PRO36587  
Figure 125: DNA325584, NP\_002005.1, 200894\_s\_at  
Figure 126: PRO59262  
Figure 127: DNA325584, NM\_002014, 200895\_s\_at  
Figure 128: PRO59262  
Figure 129: DNA272961, NP\_004485.1, 200896\_x\_at  
Figure 130: PRO61041  
Figure 131A-B: DNA329018, NP\_057165.2, 200897\_s\_at  
Figure 132: PRO84693  
Figure 133: DNA328380, X64879, 200904\_at  
Figure 134A-B: DNA329018, NM\_016081, 200907\_s\_at  
Figure 135: PRO84693  
Figure 136: DNA304665, NP\_000995.1, 200909\_s\_at  
Figure 137: PRO71092  
Figure 138: DNA272974, NP\_005989.1, 200910\_at  
Figure 139: PRO61054  
Figure 140: DNA272695, NP\_001722.1, 200920\_s\_at  
Figure 141: PRO60817  
Figure 142: DNA272695, NM\_001731, 200921\_s\_at  
Figure 143: PRO60817  
Figure 144A-B: DNA270430, NP\_054706.1, 200931\_s\_at  
Figure 145: PRO58810  
Figure 146: DNA325153, NP\_150644.1, 200936\_at  
Figure 147: PRO22907  
Figure 148: DNA329925, NP\_001528.1, 200942\_s\_at  
Figure 149: PRO85239  
Figure 150A-B: DNA287217, NP\_001750.1, 200951\_s\_at  
Figure 151: PRO36766  
Figure 152A-B: DNA287217, NM\_001759, 200952\_s\_at  
Figure 153: PRO36766  
Figure 154A-B: DNA226303, D13639, 200953\_s\_at  
Figure 155: PRO36766  
Figure 156: DNA324149, NP\_000984.1, 200963\_x\_at  
Figure 157: PRO11197  
Figure 158A-C: DNA344253, NP\_002304.2, 200965\_s\_at  
Figure 159: PRO94999  
Figure 160: DNA344254, AL137335, 200992\_at  
Figure 161: DNA325778, NP\_006816.2, 200998\_s\_at  
Figure 162: PRO82248  
Figure 163: DNA325778, NM\_006825, 200999\_s\_at  
Figure 164: PRO82248  
Figure 165: DNA275408, NP\_001596.1, 201000\_at  
Figure 166: PRO63068  
Figure 167: DNA328387, NP\_001760.1, 201005\_at  
Figure 168: PRO4769  
Figure 169: DNA304713, NP\_006463.2, 201008\_s\_at  
Figure 170: PRO71139  
Figure 171: DNA304713, NM\_006472, 201009\_s\_at  
Figure 172: PRO71139  
Figure 173: DNA304713, S73591, 201010\_s\_at  
Figure 174: PRO71139  
Figure 175: DNA89242, NP\_000691.1, 201012\_at  
Figure 176: PRO2907  
Figure 177: DNA328388, NP\_006443.1, 201014\_s\_at  
Figure 178: PRO84240  
Figure 179A-B: DNA344255, 1327792.5, 201016\_at  
Figure 180: PRO95001  
Figure 181: DNA328389, NP\_006861.1, 201022\_s\_at  
Figure 182: PRO84241  
Figure 183: DNA344256, NP\_005633.2, 201023\_at  
Figure 184: PRO95002  
Figure 185A-B: DNA329101, NP\_056988.2, 201024\_x\_at  
Figure 186: PRO84751  
Figure 187: DNA196628, NP\_005318.1, 201036\_s\_at  
Figure 188: PRO25105  
Figure 189: DNA328391, NP\_004408.1, 201041\_s\_at  
Figure 190: PRO84242  
Figure 191: DNA344257, NP\_006296.1, 201043\_s\_at  
Figure 192: PRO95003  
Figure 193: DNA103208, NP\_004090.3, 201061\_s\_at  
Figure 194: PRO4538  
Figure 195: DNA344258, NP\_003810.1, 201064\_s\_at  
Figure 196: PRO62717  
Figure 197: DNA344259, NP\_001907.2, 201066\_at  
Figure 198: PRO95004  
Figure 199: DNA151675, NP\_004791.1, 201078\_at  
Figure 200: PRO11975  
Figure 201: DNA274743, NP\_002850.1, 201087\_at  
Figure 202: PRO62517  
Figure 203: DNA254725, NP\_002257.1, 201088\_at  
Figure 204: PRO49824  
Figure 205: DNA304719, NP\_002296.1, 201105\_at  
Figure 206: PRO71145  
Figure 207: DNA344260, NP\_003312.2, 201113\_at  
Figure 208: PRO95005  
Figure 209: DNA326273, NP\_001961.1, 201123\_s\_at  
Figure 210: PRO82678  
Figure 211: DNA271185, NP\_002397.1, 201126\_s\_at  
Figure 212: PRO59502

- Figure 213: DNA344261, NP\_062543.1, 201132\_at  
Figure 214: PRO95006  
Figure 215A-B: DNA227128, NP\_055634.1, 201133\_s\_at  
Figure 216: PRO37591  
Figure 217: DNA329104, NP\_004085.1, 201144\_s\_at  
Figure 218: PRO69550  
Figure 219: DNA344262, NP\_000959.2, 201154\_x\_at  
Figure 220: PRO95007  
Figure 221A-B: DNA326365, NP\_066565.1, 201158\_at  
Figure 222: PRO82761  
Figure 223: DNA334099, NP\_003642.2, 201161\_s\_at  
Figure 224: PRO85244  
Figure 225: DNA151802, NP\_003661.1, 201169\_s\_at  
Figure 226: PRO12890  
Figure 227: DNA151802, NM\_003670, 201170\_s\_at  
Figure 228: PRO12890  
Figure 229: DNA329091, NP\_003936.1, 201171\_at  
Figure 230: PRO11997  
Figure 231: DNA323783, NP\_006591.1, 201173\_x\_at  
Figure 232: PRO80535  
Figure 233A-B: DNA344263, NP\_003477.2, 201195\_s\_at  
Figure 234: PRO49192  
Figure 235: DNA328400, NP\_003842.1, 201200\_at  
Figure 236: PRO1409  
Figure 237: DNA103488, NP\_002583.1, 201202\_at  
Figure 238: PRO4815  
Figure 239: DNA344264, NP\_005023.2, 201215\_at  
Figure 240: PRO83378  
Figure 241: DNA326974, NP\_000958.1, 201217\_x\_at  
Figure 242: PRO83285  
Figure 243: DNA327544, NP\_002865.1, 201222\_s\_at  
Figure 244: PRO70357  
Figure 245: DNA344265, NP\_006754.1, 201235\_s\_at  
Figure 246: PRO80725  
Figure 247: DNA275049, NP\_004930.1, 201241\_at  
Figure 248: PRO62770  
Figure 249: DNA226615, NP\_001668.1, 201242\_s\_at  
Figure 250: PRO37078  
Figure 251: DNA226615, NM\_001677, 201243\_s\_at  
Figure 252: PRO37078  
Figure 253: DNA287331, NP\_002645.1, 201251\_at  
Figure 254: PRO69595  
Figure 255: DNA324525, NP\_000997.1, 201257\_x\_at  
Figure 256: PRO81179  
Figure 257: DNA227416, NP\_006745.1, 201259\_s\_at  
Figure 258: PRO37879  
Figure 259: DNA227416, NM\_006754, 201260\_s\_at  
Figure 260: PRO37879  
Figure 261: DNA270950, NP\_003182.1, 201263\_at  
Figure 262: PRO59281  
Figure 263: DNA97290, NP\_002503.1, 201268\_at  
Figure 264: PRO3637  
Figure 265: DNA344266, AF267863, 201276\_at  
Figure 266: PRO95008  
Figure 267: DNA328405, NP\_112556.1, 201277\_s\_at  
Figure 268: PRO84252  
Figure 269: DNA331290, NP\_038474.1, 201285\_at  
Figure 270: PRO86391  
Figure 271: DNA270526, NP\_001166.1, 201288\_at  
Figure 272: PRO58903  
Figure 273A-B: DNA327545, NP\_001058.2, 201291\_s\_at  
Figure 274: PRO82731  
Figure 275A-B: DNA327545, NM\_001067, 201292\_at  
Figure 276: PRO82731  
Figure 277A-B: DNA344267, NM\_134264, 201294\_s\_at  
Figure 278: PRO95009  
Figure 279A-B: DNA226778, AL110269, 201295\_s\_at  
Figure 280: PRO37241  
Figure 281: DNA333423, NP\_001144.1, 201301\_s\_at  
Figure 282: PRO61325  
Figure 283: DNA333423, NM\_001153, 201302\_at  
Figure 284: PRO61325  
Figure 285: DNA329106, NP\_003013.1, 201311\_s\_at  
Figure 286: PRO83360  
Figure 287: DNA329106, NM\_003022, 201312\_s\_at  
Figure 288: PRO83360  
Figure 289: DNA255078, NP\_006426.1, 201315\_x\_at  
Figure 290: PRO50165  
Figure 291: DNA274745, NP\_006815.1, 201323\_at  
Figure 292: PRO62518  
Figure 293: DNA150781, NP\_001414.1, 201324\_at  
Figure 294: PRO12467  
Figure 295: DNA150781, NM\_001423, 201325\_s\_at  
Figure 296: PRO12467  
Figure 297: DNA329002, NP\_001753.1, 201326\_at  
Figure 298: PRO4912  
Figure 299: DNA329002, NM\_001762, 201327\_s\_at  
Figure 300: PRO4912  
Figure 301A-C: DNA271656, NP\_056128.1, 201334\_s\_at  
Figure 302: PRO59943  
Figure 303: DNA329107, NP\_008818.3, 201367\_s\_at  
Figure 304: PRO84754  
Figure 305A-B: DNA329108, 1383643.16, 201368\_at  
Figure 306: PRO84755  
Figure 307: DNA329107, NM\_006887, 201369\_s\_at  
Figure 308: PRO84754  
Figure 309: DNA329218, NP\_055227.1, 201381\_x\_at  
Figure 310: PRO84829  
Figure 311: DNA344268, NP\_002800.2, 201388\_at  
Figure 312: PRO63269  
Figure 313: DNA326116, NP\_057376.1, 201391\_at  
Figure 314: PRO82542  
Figure 315: DNA331447, NP\_006614.2, 201397\_at  
Figure 316: PRO85247  
Figure 317: DNA328410, NP\_004519.1, 201403\_s\_at  
Figure 318: PRO60174  
Figure 319: DNA327072, NP\_066357.1, 201406\_at

- Figure 320: PRO10723  
Figure 321: DNA344269, NP\_077007.1, 201420\_s\_at  
Figure 322: PRO95010  
Figure 323: DNA272286, NP\_001743.1, 201432\_at  
Figure 324: PRO60544  
Figure 325A-C: DNA88140, NP\_004360.1, 201438\_at  
Figure 326: PRO2670  
Figure 327: DNA344270, NP\_071505.1, 201450\_s\_at  
Figure 328: PRO95011  
Figure 329: DNA326736, NP\_006657.1, 201459\_at  
Figure 330: PRO83076  
Figure 331: DNA226359, NP\_002219.1, 201464\_x\_at  
Figure 332: PRO36822  
Figure 333: DNA226359, NM\_002228, 201466\_s\_at  
Figure 334: PRO36822  
Figure 335: DNA328414, NP\_003891.1, 201471\_s\_at  
Figure 336: PRO81346  
Figure 337: DNA103320, NP\_002220.1, 201473\_at  
Figure 338: PRO4650  
Figure 339: DNA325704, NP\_004981.2, 201475\_x\_at  
Figure 340: PRO82188  
Figure 341: DNA327551, NP\_001024.1, 201476\_s\_at  
Figure 342: PRO59289  
Figure 343: DNA327551, NM\_001033, 201477\_s\_at  
Figure 344: PRO59289  
Figure 345: DNA254783, NP\_001354.1, 201478\_s\_at  
Figure 346: PRO49881  
Figure 347: DNA254783, NM\_001363, 201479\_at  
Figure 348: PRO49881  
Figure 349: DNA329940, NP\_001805.1, 201487\_at  
Figure 350: PRO2679  
Figure 351: DNA304459, NP\_005720.1, 201489\_at  
Figure 352: PRO37073  
Figure 353: DNA304459, NM\_005729, 201490\_s\_at  
Figure 354: PRO37073  
Figure 355: DNA325920, NP\_036243.1, 201491\_at  
Figure 356: PRO82373  
Figure 357: DNA253807, NP\_065390.1, 201502\_s\_at  
Figure 358: PRO49210  
Figure 359: DNA329941, NP\_001543.1, 201508\_at  
Figure 360: PRO85249  
Figure 361: DNA323741, NP\_003123.1, 201516\_at  
Figure 362: PRO80498  
Figure 363: DNA344271, NP\_073719.1, 201522\_x\_at  
Figure 364: PRO62659  
Figure 365: DNA328418, NP\_003398.1, 201531\_at  
Figure 366: PRO84261  
Figure 367: DNA329943, NP\_009037.1, 201534\_s\_at  
Figure 368: PRO85251  
Figure 369: DNA329943, NM\_007106, 201535\_at  
Figure 370: PRO85251  
Figure 371: DNA329553, NP\_064535.1, 201543\_s\_at  
Figure 372: PRO38313  
Figure 373: DNA344272, NP\_004121.2, 201554\_x\_at  
Figure 374: PRO95012  
Figure 375: DNA272171, NP\_002379.2, 201555\_at  
Figure 376: PRO60438  
Figure 377: DNA226291, NP\_055047.1, 201557\_at  
Figure 378: PRO36754  
Figure 379A-B: DNA290226, NP\_039234.1, 201559\_s\_at  
Figure 380: PRO70317  
Figure 381A-B: DNA290226, NM\_013943, 201560\_at  
Figure 382: PRO70317  
Figure 383: DNA227478, NP\_002157.1, 201565\_s\_at  
Figure 384: PRO37941  
Figure 385: DNA150986, D13891, 201566\_x\_at  
Figure 386: PRO0  
Figure 387: DNA344273, M75715, 201573\_s\_at  
Figure 388: PRO95013  
Figure 389A-B: DNA270995, NP\_004721.1, 201574\_at  
Figure 390: PRO59324  
Figure 391: DNA227071, NP\_000260.1, 201577\_at  
Figure 392: PRO37534  
Figure 393A-B: DNA329944, AB032988, 201581\_at  
Figure 394: DNA227013, NP\_001560.1, 201587\_s\_at  
Figure 395: PRO37476  
Figure 396: DNA150990, NP\_003632.1, 201601\_x\_at  
Figure 397: PRO12570  
Figure 398: DNA290280, NP\_004359.1, 201605\_x\_at  
Figure 399: PRO70425  
Figure 400: DNA329947, NP\_536806.1, 201613\_s\_at  
Figure 401: PRO37674  
Figure 402: DNA188207, NM\_005380, 201621\_at  
Figure 403: PRO21719  
Figure 404: DNA329114, NP\_001340.1, 201623\_s\_at  
Figure 405: PRO84759  
Figure 406: DNA329114, NM\_001349, 201624\_at  
Figure 407: PRO84759  
Figure 408: DNA344274, 7698185.18, 201626\_at  
Figure 409: PRO95014  
Figure 410A-D: DNA344275, U96876, 201627\_s\_at  
Figure 411: DNA344276, NM\_004300, 201629\_s\_at  
Figure 412: PRO89350  
Figure 413: DNA329115, NP\_434702.1, 201631\_s\_at  
Figure 414: PRO84760  
Figure 415: DNA326193, NP\_085056.1, 201634\_s\_at  
Figure 416: PRO82609  
Figure 417: DNA287240, NP\_004326.1, 201641\_at  
Figure 418: PRO29371  
Figure 419: DNA88410, NP\_005525.1, 201642\_at  
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Figure 423: DNA328423, NP\_003245.1, 201666\_at  
Figure 424: PRO2121  
Figure 425: DNA344277, NP\_683877.1, 201676\_x\_at  
Figure 426: PRO81959  
Figure 427: DNA324742, NP\_001751.1, 201700\_at  
Figure 428: PRO81367  
Figure 429: DNA270883, NP\_001061.1, 201714\_at  
Figure 430: PRO59218

- Figure 431A-B: DNA151806, NP\_001422.1, 201718\_s\_at  
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Figure 433A-B: DNA151806, NM\_001431, 201719\_s\_at  
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Figure 436: PRO61721  
Figure 437: DNA344278, NP\_005618.2, 201739\_at  
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Figure 439: DNA326373, NP\_008855.1, 201742\_x\_at  
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Figure 444: PRO59136  
Figure 445A-B: DNA150444, NP\_055589.1, 201778\_s\_at  
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Figure 447A-B: DNA103387, NP\_002287.1, 201795\_at  
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Figure 457: DNA329952, NP\_005854.2, 201830\_s\_at  
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Figure 462: PRO2795  
Figure 463: DNA254350, NP\_004043.2, 201849\_at  
Figure 464: PRO49461  
Figure 465: DNA150725, NP\_001738.1, 201850\_at  
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Figure 481: PRO45093  
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Figure 498: DNA83046, NM\_000574, 201926\_s\_at  
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- Figure 537: PRO84274  
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Figure 591: PRO1213  
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Figure 603A-B: DNA269642, NP\_004557.1, 202464\_s\_at  
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Figure 605: DNA227921, NP\_003789.1, 202468\_s\_at  
Figure 606: PRO38384  
Figure 607A-B: DNA329122, NP\_067675.1, 202478\_at  
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Figure 609A-B: DNA329122, NM\_021643, 202479\_s\_at  
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Figure 614: PRO95022  
Figure 615: DNA324925, NP\_036544.1, 202487\_s\_at  
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Figure 622: PRO38852  
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Figure 625A-B: DNA277809, NM\_014767, 202524\_s\_at  
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Figure 635: DNA325587, NP\_068772.1, 202580\_x\_at

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 Figure 658: PRO160  
 Figure 659: DNA289528, NP\_004302.1, 202641\_at  
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 Figure 665: DNA254129, NP\_006001.1, 202655\_at  
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 Figure 688: PRO58642  
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 Figure 698: PRO1189  
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 Figure 702: PRO37627  
 Figure 703A-C: DNA329129, NP\_009134.1, 202759\_s\_at  
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 Figure 707A-B: DNA256782, AL080133, 202761\_s\_at  
 Figure 708: PRO51715  
 Figure 709A-B: DNA328464, 977954.20, 202769\_at  
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 Figure 712: PRO37041  
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 Figure 714: PRO61349  
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 Figure 716: PRO63011  
 Figure 717: DNA344305, 345245.28, 202789\_at  
 Figure 718: PRO95030  
 Figure 719: DNA329986, NP\_006454.1, 202811\_at  
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 Figure 723: DNA269828, NP\_006691.1, 202837\_at  
 Figure 724: PRO58230  
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 Figure 726: PRO1471  
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 Figure 728: PRO1471  
 Figure 729: DNA328466, NP\_004554.1, 202847\_at  
 Figure 730: PRO84292  
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 Figure 732: PRO37526  
 Figure 733: DNA103394, NP\_004198.1, 202855\_s\_at  
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 Figure 735: DNA103394, NM\_004207, 202856\_s\_at  
 Figure 736: PRO4722  
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 Figure 738: PRO74  
 Figure 739: DNA275144, NP\_000128.1, 202862\_at  
 Figure 740: PRO62852

- Figure 741: DNA328467, NP\_003104.2, 202864.s.at  
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Figure 744: PRO69559  
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Figure 747: DNA325334, NP\_061931.1, 202887.s.at  
Figure 748: PRO81877  
Figure 749A-B: DNA333705, NP\_004070.3, 202901.x.at  
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Figure 753: DNA332688, NP\_510966.1, 202910.s.at  
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Figure 755A-B: DNA275066, NP\_000170.1, 202911.at  
Figure 756: PRO62786  
Figure 757: DNA83008, NP\_001115.1, 202912.at  
Figure 758: PRO2032  
Figure 759A-B: DNA344307, 7762119.3, 202934.at  
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Figure 761: DNA344308, NP\_056518.2, 202937.x.at  
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Figure 766: PRO57901  
Figure 767: DNA273320, NP\_008950.1, 202954.at  
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Figure 772: PRO84772  
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Figure 776: PRO2611  
Figure 777A-B: DNA344310, NP\_055566.1, 203037.s.at  
Figure 778: PRO95034  
Figure 779A-B: DNA344311, NP\_002835.2, 203038.at  
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Figure 783A-B: DNA328358, NP\_005981.1, 203047.at  
Figure 784: PRO84218  
Figure 785A-B: DNA227821, NP\_055666.1, 203068.at  
Figure 786: PRO38284  
Figure 787: DNA329137, NP\_005892.1, 203077.s.at  
Figure 788: PRO12879  
Figure 789A-B: DNA339385, NP\_055568.1, 203082.at  
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Figure 791: DNA344312, 1386457.26, 203086.at  
Figure 792: PRO95036  
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Figure 794: PRO84773  
Figure 795: DNA344313, AF026030, 203092.at  
Figure 796: PRO95037  
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Figure 799: DNA329992, NP\_002399.1, 203102.s.at  
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Figure 801: DNA272867, NP\_003960.1, 203109.at  
Figure 802: PRO60960  
Figure 803: DNA150430, NP\_006387.1, 203114.at  
Figure 804: PRO12770  
Figure 805: DNA329994, NP\_004707.2, 203118.at  
Figure 806: PRO85286  
Figure 807: DNA287417, NP\_077003.1, 203119.at  
Figure 808: PRO69674  
Figure 809A-B: DNA226395, NP\_000312.1, 203132.at  
Figure 810: PRO36858  
Figure 811A-B: DNA344314, NP\_620309.1, 203140.at  
Figure 812: PRO12790  
Figure 813: DNA269433, NP\_005877.1, 203163.at  
Figure 814: PRO57856  
Figure 815: DNA340116, NP\_000146.2, 203179.at  
Figure 816: PRO91615  
Figure 817A-B: DNA331303, NP\_003129.1, 203182.s.at  
Figure 818: PRO86399  
Figure 819: DNA304720, NP\_062427.1, 203186.s.at  
Figure 820: PRO71146  
Figure 821A-B: DNA270861, NP\_001371.1, 203187.at  
Figure 822: PRO59198  
Figure 823A-B: DNA344315, AAL56659.1, 203194.s.at  
Figure 824: PRO95038  
Figure 825: DNA329997, NP\_031396.1, 203209.at  
Figure 826: PRO61115  
Figure 827A-B: DNA328481, NP\_057240.1, 203211.s.at  
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Figure 830: PRO83607  
Figure 831: DNA334914, NP\_001777.1, 203214.x.at  
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Figure 833A-C: DNA274481, NP\_000323.1, 203231.s.at  
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Figure 835A-C: DNA274481, NM\_000332, 203232.s.at  
Figure 836: PRO62384  
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Figure 838: PRO2540  
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Figure 841: DNA334781, NM\_006457, 203243.s.at  
Figure 842: PRO89234  
Figure 843: DNA330000, NP\_036277.1, 203270.at

- Figure 844: PRO85289  
Figure 845: DNA270963, NM\_003335, 203281\_s\_at  
Figure 846: PRO59293  
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Figure 849: DNA225675, NM\_005570, 203294\_s\_at  
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Figure 852: PRO84314  
Figure 853: DNA344316, NP\_733796.1, 203313\_s\_at  
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Figure 855: DNA271740, NP\_003085.1, 203316\_s\_at  
Figure 856: PRO60024  
Figure 857A-B: DNA330003, NP\_005532.1, 203331\_s\_at  
Figure 858: PRO85291  
Figure 859A-B: DNA330003, NM\_005541, 203332\_s\_at  
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Figure 861: DNA330004, NP\_055785.2, 203333\_at  
Figure 862: PRO85292  
Figure 863: DNA324514, NP\_002349.1, 203362\_s\_at  
Figure 864: PRO81169  
Figure 865: DNA328493, NP\_008957.1, 203367\_at  
Figure 866: PRO84317  
Figure 867: DNA151022, NP\_001336.1, 203385\_at  
Figure 868: PRO12096  
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Figure 871A-B: DNA340155, NP\_055647.1, 203387\_s\_at  
Figure 872: PRO91654  
Figure 873: DNA331200, NP\_004304.1, 203388\_at  
Figure 874: PRO86322  
Figure 875: DNA88324, M65128, 203391\_at  
Figure 876: PRO2748  
Figure 877A-B: DNA254616, NP\_004473.1, 203397\_s\_at  
Figure 878: PRO49718  
Figure 879: DNA270134, NP\_000098.1, 203409\_at  
Figure 880: PRO58523  
Figure 881: DNA344318, NP\_733821.1, 203411\_s\_at  
Figure 882: PRO95041  
Figure 883: DNA28759, NP\_006150.1, 203413\_at  
Figure 884: PRO2520  
Figure 885A-B: DNA256807, NP\_057339.1, 203420\_at  
Figure 886: PRO51738  
Figure 887: DNA327808, NP\_002961.1, 203455\_s\_at  
Figure 888: PRO83769  
Figure 889: DNA269591, NP\_002655.1, 203471\_s\_at  
Figure 890: PRO58004  
Figure 891: DNA150959, NP\_005813.1, 203498\_at  
Figure 892: PRO11599  
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Figure 906: PRO60997  
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Figure 920: PRO83611  
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Figure 927: DNA329033, NP\_005375.1, 203574\_at  
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Figure 929: DNA344323, NP\_054763.2, 203583\_at  
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Figure 1298: PRO95069  
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Figure 1328: PRO313  
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Figure 1340: PRO90913  
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Figure 1352: PRO23370

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- Figure 1454: PRO91128  
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- Figure 1554: PRO60433  
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- Figure 1658: PRO84511  
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- Figure 1758: PRO80934  
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Figure 1828: PRO36134  
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Figure 1831: DNA330145, NP\_002788.1, 208799\_at  
Figure 1832: PRO84403  
Figure 1833A-C: DNA330146, 1397486.26, 208806\_at  
Figure 1834: PRO85404  
Figure 1835: DNA273521, NP\_002070.1, 208813\_at  
Figure 1836: PRO61502  
Figure 1837: DNA327699, BAA75062.1, 208815\_x\_at  
Figure 1838: PRO83682  
Figure 1839: DNA344435, NP\_002789.1, 208827\_at  
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Figure 1842: PRO2564  
Figure 1843: DNA227874, NP\_003320.1, 208864\_s\_at  
Figure 1844: PRO38337  
Figure 1845: DNA344436, NP\_113600.1, 208869\_s\_at  
Figure 1846: PRO95105  
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Figure 1848: PRO59076  
Figure 1849: DNA270713, NP\_001937.1, 208892\_s\_at  
Figure 1850: PRO59076  
Figure 1851: DNA328625, NM\_022652, 208893\_s\_at  
Figure 1852: PRO84404  
Figure 1853: DNA329221, NP\_061984.1, 208894\_at  
Figure 1854: PRO4555  
Figure 1855A-B: DNA324910, NP\_061820.1, 208905\_at  
Figure 1856: PRO81514  
Figure 1857: DNA326260, NP\_001203.1, 208910\_s\_at  
Figure 1858: PRO82667  
Figure 1859: DNA226500, NP\_005619.1, 208916\_at  
Figure 1860: PRO36963  
Figure 1861: DNA325473, NP\_006353.2, 208922\_s\_at  
Figure 1862: PRO81996

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Figure 1864: PRO85097  
Figure 1865: DNA326233, NP\_000968.2, 208929\_x\_at  
Figure 1866: PRO82645  
Figure 1867: DNA327702, NP\_006490.2, 208934\_s\_at  
Figure 1868: PRO83684  
Figure 1869: DNA327702, NM\_006499, 208936\_x\_at  
Figure 1870: PRO83684  
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Figure 1872: PRO70339  
Figure 1873A-B: DNA344438, D50683, 208944\_at  
Figure 1874: PRO95106  
Figure 1875: DNA325900, NP\_002297.1, 208949\_s\_at  
Figure 1876: PRO82356  
Figure 1877: DNA327661, NP\_005522.1, 208966\_x\_at  
Figure 1878: PRO83652  
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Figure 1886: PRO85080  
Figure 1887: DNA330155, 7692317.2, 208982\_at  
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Figure 1894: PRO95107  
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Figure 1896: PRO86548  
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Figure 1898: PRO38015  
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Figure 1900: PRO95108  
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Figure 1902: PRO84408  
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Figure 1906: PRO84410  
Figure 1907: DNA328633, NP\_004784.2, 209017\_s\_at  
Figure 1908: PRO84411  
Figure 1909: DNA327706, NP\_006363.3, 209024\_s\_at  
Figure 1910: PRO83688  
Figure 1911: DNA344442, AF279899, 209034\_at  
Figure 1912: PRO95109  
Figure 1913: DNA274967, AF233453, 209049\_s\_at  
Figure 1914: PRO62700  
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Figure 1916: PRO81109  
Figure 1917A-B: DNA331518, NM\_133336, 209053\_s\_at  
Figure 1918: PRO86550  
Figure 1919A-B: DNA226405, NM\_006534, 209060\_x\_at  
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Figure 1922: PRO95110  
Figure 1923A-B: DNA226405, AF036892, 209062\_x\_at  
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Figure 1928: PRO84814  
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Figure 1930: PRO81135  
Figure 1931A-B: DNA273483, AB007960, 209090\_s\_at  
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Figure 1943: PRO95113  
Figure 1944: DNA344448, NM\_176895, 209147\_s\_at  
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Figure 1946: DNA330166, NP\_004688.2, 209161\_at  
Figure 1947: PRO85418  
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Figure 1955: PRO84815  
Figure 1956A-B: DNA344451, NP\_733765.1, 209186\_at  
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Figure 2007: PRO85423  
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Figure 2009: PRO91131  
Figure 2010: DNA330175, NP\_006836.1, 209408\_at  
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Figure 2021: PRO69571  
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Figure 2029: PRO81503  
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Figure 2035: PRO82426  
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Figure 2037: PRO62684  
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Figure 2039: PRO83388  
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Figure 2041: PRO19618  
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Figure 2065: PRO85434

- Figure 2066: DNA323856, NP\_056455.1, 209669\_s\_at  
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Figure 2091: PRO62893  
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Figure 2097: PRO90442  
Figure 2098: DNA226436, NP\_001772.1, 209795\_at  
Figure 2099: PRO36899  
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Figure 2111: PRO61686  
Figure 2112: DNA327732, NP\_036606.2, 209825\_s\_at  
Figure 2113: PRO61801  
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Figure 2122: PRO95137  
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Figure 2124: PRO81419  
Figure 2125: DNA272753, NP\_005780.1, 209853\_s\_at  
Figure 2126: PRO60864  
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Figure 2128: PRO61513  
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Figure 2130: PRO82238  
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Figure 2132: PRO36583  
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Figure 2138: PRO80882  
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Figure 2142: PRO70858  
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Figure 2154: DNA226658, NM\_003745, 210001\_s\_at  
Figure 2155: PRO37121  
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Figure 2157: PRO95140  
Figure 2158A-B: DNA344487, NM\_006785, 210018\_x\_at  
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Figure 2161: PRO50974  
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Figure 2165: PRO83142  
Figure 2166: DNA328285, NP\_002745.1, 210059\_s\_at

- Figure 2167: PRO84161  
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Figure 2175: PRO49421  
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Figure 2183: PRO51063  
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Figure 2189: PRO19838  
Figure 2190: DNA287620, NP\_004122.1, 210164\_at  
Figure 2191: PRO2081  
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Figure 2193: PRO89492  
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Figure 2195: PRO85449  
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Figure 2199: PRO1756  
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Figure 2205: PRO59660  
Figure 2206: DNA287333, NP\_005283.1, 210279\_at  
Figure 2207: PRO69597  
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Figure 2209: PRO58410  
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Figure 2211: PRO24078  
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Figure 2213: PRO60406  
Figure 2214A-B: DNA188419, NP\_002011.1, 210316\_at  
Figure 2215: PRO21767  
Figure 2216: DNA329213, NP\_219491.1, 210321\_at  
Figure 2217: PRO2313  
Figure 2218: DNA225528, NP\_000610.1, 210354\_at  
Figure 2219: PRO35991  
Figure 2220: DNA330207, BC001131, 210387\_at  
Figure 2221: PRO85451  
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Figure 2223: PRO85452  
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Figure 2225: PRO95143  
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Figure 2227: PRO7424  
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Figure 2235: PRO80599  
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Figure 2237: PRO62367  
Figure 2238: DNA344499, NM\_134262, 210479\_s\_at  
Figure 2239: PRO95145  
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Figure 2245: PRO50891  
Figure 2246: DNA270066, AF078844, 210524\_x\_at  
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Figure 2249: PRO95146  
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Figure 2253: PRO82622  
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Figure 2255: PRO95147  
Figure 2256: DNA344506, NM\_172211, 210557\_x\_at  
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Figure 2259: PRO70806  
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Figure 2269: PRO38185  
Figure 2270: DNA330210, U03858, 210607\_at  
Figure 2271: PRO126  
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- Figure 2273: PRO11557  
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Figure 2283: PRO51556  
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Figure 2293: PRO4575  
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- Figure 2377: DNA327754, NP\_150634.1, 211367\_s\_at  
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- Figure 2481: PRO4904  
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- Figure 2580: PRO85484  
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Figure 2588: PRO11726  
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Figure 2590: PRO95195  
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Figure 2628: DNA331298, NM\_014456, 212593\_s\_at  
Figure 2629: PRO81909  
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Figure 2633: PRO95204  
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Figure 2639: PRO23989  
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Figure 2647: PRO84699  
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Figure 2649: PRO83789  
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Figure 2653: PRO84830  
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Figure 2663: PRO83744  
Figure 2664A-B: DNA273398, NM\_015568, 212750\_at  
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Figure 2669: PRO95213  
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Figure 2674: PRO12281  
Figure 2675A-B: DNA344597, NP\_055894.1, 212796\_s\_at  
Figure 2676: PRO95215  
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- Figure 2678: PRO84500  
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 Figure 2683: PRO85421  
 Figure 2684: DNA344599, 234498.36, 212847.at  
 Figure 2685: PRO95217  
 Figure 2686: DNA344600, AL713742, 212886.at  
 Figure 2687: PRO95218  
 Figure 2688: DNA344601, 989341.96, 212906.at  
 Figure 2689: PRO85986  
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 Figure 2692: PRO61023  
 Figure 2693: DNA344602, BC045715, 212923.s.at  
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 Figure 2698: PRO80842  
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 Figure 2702: DNA325417, NP\_001742.1, 212971.at  
 Figure 2703: PRO69635  
 Figure 2704A-B: DNA344606, 474311.10, 212985.at  
 Figure 2705: PRO95220  
 Figure 2706: DNA344607, NM\_147156, 212989.at  
 Figure 2707: PRO50467  
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 Figure 2712: PRO49218  
 Figure 2713A-B: DNA344609, NM\_174953,  
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 Figure 2715: DNA344610, NP\_699172.1, 213038.at  
 Figure 2716: PRO95222  
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 213056.at  
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 Figure 2722: PRO84506  
 Figure 2723: DNA150837, CAA06743.1, 213083.at  
 Figure 2724: PRO12495  
 Figure 2725: DNA344611, NP\_000975.2, 213084.x.at  
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 213111.at  
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 Figure 2733: PRO24295  
 Figure 2734: DNA326217, NP\_004474.1, 213129.s.at  
 Figure 2735: PRO82630  
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 Figure 2738: DNA287230, AAA36325.1, 213138.at  
 Figure 2739: PRO69509  
 Figure 2740: DNA330277, CAB45152.1, 213142.x.at  
 Figure 2741: PRO85506  
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 Figure 2745: PRO95226  
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 Figure 2748: PRO95227  
 Figure 2749: DNA339710, NP\_116167.3, 213189.at  
 Figure 2750: PRO91439  
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 Figure 2753: PRO95229  
 Figure 2754: DNA344619, 1398007.8, 213226.at  
 Figure 2755: PRO95230  
 Figure 2756A-B: DNA344620, NP\_065186.2,  
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 Figure 2757: PRO95231  
 Figure 2758A-B: DNA194850, BAA25458.1,  
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 Figure 2759: PRO24112  
 Figure 2760A-C: DNA344621, BAA20800.2,  
 213261.at  
 Figure 2761: PRO59767  
 Figure 2762A-B: DNA344622, AY217548, 213281.at  
 Figure 2763: PRO4671  
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- Figure 2775: PRO95234  
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Figure 2786: PRO95237  
Figure 2787A-B: DNA344629, 7697344.6, 213416\_at  
Figure 2788: PRO95238  
Figure 2789A-B: DNA331398, DNA331398, 213457\_at  
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- Figure 2877: PRO95255  
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Figure 2879: PRO95256  
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Figure 2979: PRO23844  
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Figure 2981: PRO95276

- Figure 2982A-B: DNA344680, NM\_015184, 216218.s.at  
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 Figure 2989: PRO95279  
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 Figure 2994: PRO69518  
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 Figure 3008: PRO2557  
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 Figure 3049: PRO95290  
 Figure 3050: DNA344696, 346253.1, 217550.at  
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 Figure 3058: DNA325832, NM\_021999, 217732.s.at  
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 Figure 3076A-B: DNA254292, NM\_004481, 217788.s.at  
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 Figure 3081: PRO95294  
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 Figure 3086: DNA344702, NP\_066952.1, 217848.s.at

- Figure 3087: PRO11669  
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Figure 3090: DNA344703, NP\_002686.2, 217854\_s\_at  
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Figure 3093: PRO95297  
Figure 3094: DNA335592, NP\_036237.2, 217867\_x\_at  
Figure 3095: PRO852  
Figure 3096: DNA344705, NP\_001247.2, 217879\_at  
Figure 3097: PRO95298  
Figure 3098: DNA255145, NP\_060917.1, 217882\_at  
Figure 3099: PRO50225  
Figure 3100A-B: DNA325652, NP\_057441.1, 217892\_s\_at  
Figure 3101: PRO82143  
Figure 3102: DNA330345, NP\_055130.1, 217906\_at  
Figure 3103: PRO85566  
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Figure 3106: DNA344706, NP\_751918.1, 217919\_s\_at  
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Figure 3108: DNA287241, NP\_056991.1, 217933\_s\_at  
Figure 3109: PRO69516  
Figure 3110A-B: DNA225648, NP\_061165.1, 217941\_s\_at  
Figure 3111: PRO36111  
Figure 3112: DNA326730, NP\_057037.1, 217950\_at  
Figure 3113: PRO83072  
Figure 3114: DNA329273, NP\_037374.1, 217957\_at  
Figure 3115: PRO84869  
Figure 3116A-B: DNA272661, NP\_443198.1, 217966\_s\_at  
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Figure 3118A-B: DNA272661, NM\_052966, 217967\_s\_at  
Figure 3119: PRO60787  
Figure 3120: DNA329546, NP\_055214.1, 217979\_at  
Figure 3121: PRO296  
Figure 3122: DNA227218, NP\_003721.2, 217983\_s\_at  
Figure 3123: PRO37681  
Figure 3124: DNA227218, NM\_003730, 217984\_at  
Figure 3125: PRO37681  
Figure 3126: DNA328831, NP\_057329.1, 217989\_at  
Figure 3127: PRO233  
Figure 3128: DNA344707, NP\_663768.1, 217991\_x\_at  
Figure 3129: PRO95300  
Figure 3130: DNA328832, NP\_067022.1, 217995\_at  
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Figure 3132: DNA328833, BC018929, 217996\_at  
Figure 3133: PRO84569  
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Figure 3136: PRO69625  
Figure 3137: DNA326005, NP\_057004.1, 218007\_s\_at  
Figure 3138: PRO82446  
Figure 3139: DNA273008, NP\_003972.1, 218009\_s\_at  
Figure 3140: PRO61079  
Figure 3141: DNA339506, NP\_060589.1, 218016\_s\_at  
Figure 3142: PRO91277  
Figure 3143: DNA325094, NP\_079346.1, 218017\_s\_at  
Figure 3144: PRO81671  
Figure 3145: DNA328836, NP\_054894.1, 218027\_at  
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Figure 3147A-B: DNA255183, NP\_061900.1, 218035\_s\_at  
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Figure 3149: DNA325978, NM\_016359, 218039\_at  
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Figure 3156: PRO81734  
Figure 3157: DNA344708, NP\_056207.2, 218086\_at  
Figure 3158: PRO95301  
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Figure 3160: PRO84871  
Figure 3161: DNA225639, NP\_060831.1, 218096\_at  
Figure 3162: PRO36102  
Figure 3163: DNA344709, NP\_004540.1, 218101\_s\_at  
Figure 3164: PRO82036  
Figure 3165: DNA344710, NP\_666499.1, 218105\_s\_at  
Figure 3166: PRO62669  
Figure 3167: DNA344711, NP\_060699.2, 218139\_s\_at  
Figure 3168: PRO95302  
Figure 3169: DNA327857, NP\_057386.1, 218142\_s\_at  
Figure 3170: PRO83799  
Figure 3171: DNA287235, NP\_060598.1, 218156\_s\_at  
Figure 3172: PRO69514  
Figure 3173: DNA151377, NP\_057132.1, 218170\_at  
Figure 3174: PRO11754  
Figure 3175: DNA304470, NP\_061100.1, 218172\_s\_at  
Figure 3176: PRO71046  
Figure 3177A-D: DNA340174, NP\_064630.1, 218184\_at  
Figure 3178: PRO91669  
Figure 3179: DNA344712, NP\_036590.1, 218188\_s\_at  
Figure 3180: PRO82887  
Figure 3181A-C: DNA330360, NP\_078789.1, 218204\_s\_at  
Figure 3182: PRO85576  
Figure 3183: DNA344713, NP\_060641.2, 218218\_at  
Figure 3184: PRO95303  
Figure 3185: DNA225650, NP\_057246.1, 218234\_at  
Figure 3186: PRO36113  
Figure 3187: DNA327858, NP\_036473.1, 218238\_at  
Figure 3188: PRO83800  
Figure 3189: DNA327858, NM\_012341, 218239\_s\_at  
Figure 3190: PRO83800

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Figure 3193: DNA329074, NP\_064524.1, 218285\_s\_at  
Figure 3194: PRO21326  
Figure 3195A-B: DNA328853, NP\_065702.2, 218319\_at  
Figure 3196: PRO84584  
Figure 3197: DNA329281, NP\_036526.2, 218336\_at  
Figure 3198: PRO84874  
Figure 3199A-B: DNA344715, BAB47444.2, 218342\_s\_at  
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Figure 3203A-B: DNA273415, NP\_036442.2, 218355\_at  
Figure 3204: PRO61414  
Figure 3205: DNA344716, NP\_071921.1, 218373\_at  
Figure 3206: PRO95306  
Figure 3207A-B: DNA330366, NP\_073602.2, 218376\_s\_at  
Figure 3208: PRO85581  
Figure 3209: DNA328856, NP\_068376.1, 218380\_at  
Figure 3210: PRO84586  
Figure 3211: DNA327863, NP\_055131.1, 218384\_at  
Figure 3212: PRO83804  
Figure 3213: DNA255340, NP\_060154.1, 218396\_at  
Figure 3214: PRO50409  
Figure 3215: DNA344717, NP\_663747.1, 218399\_s\_at  
Figure 3216: PRO95307  
Figure 3217A-B: DNA287192, NP\_006178.1, 218400\_at  
Figure 3218: PRO69478  
Figure 3219: DNA333245, NP\_037454.2, 218404\_at  
Figure 3220: PRO87952  
Figure 3221A-B: DNA344718, NP\_076414.2, 218456\_at  
Figure 3222: PRO95308  
Figure 3223: DNA328861, NP\_057030.2, 218472\_s\_at  
Figure 3224: PRO84589  
Figure 3225: DNA327943, NP\_055399.1, 218498\_s\_at  
Figure 3226: PRO865  
Figure 3227: DNA150648, NP\_037464.1, 218507\_at  
Figure 3228: PRO11576  
Figure 3229: DNA326550, NP\_057663.1, 218529\_at  
Figure 3230: PRO224  
Figure 3231: DNA327868, NP\_060601.2, 218542\_at  
Figure 3232: PRO83809  
Figure 3233: DNA255113, NP\_073587.1, 218543\_s\_at  
Figure 3234: PRO50195  
Figure 3235: DNA330373, NP\_060751.1, 218552\_at  
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Figure 3603: DNA344765, NP\_112487.1, 221434.s.at

- Figure 3604: PRO70013  
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Figure 3645: DNA344771, AF094508, 221681.s.at  
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Figure 3695A-B: DNA339979, BAA95990.1, 222139.s.at  
Figure 3696: PRO91487  
Figure 3697: DNA329916, 338326.15, 222142.s.at  
Figure 3698: PRO85231  
Figure 3699A-B: DNA344783, 027987.100, 222145.s.at  
Figure 3700: PRO95355  
Figure 3701: DNA331386, AL079297, 222150.s.at  
Figure 3702: DNA328975, NP\_078807.1, 222155.s.at  
Figure 3703: PRO47688  
Figure 3704: DNA256784, NP\_075069.1, 222209.s.at  
Figure 3705: PRO51716  
Figure 3706: DNA323915, NP\_077306.1, 222217.s.at  
Figure 3707: PRO703

- Figure 3708: DNA287425, NP\_060979.1, 222231.s.at  
Figure 3709: PRO69682  
Figure 3710: DNA344784, AAB26149.1, 222247.at  
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Figure 3712: DNA344785, AL137750, 222262.s.at  
Figure 3713: PRO95357  
Figure 3714: DNA344786, 405457.25, 222303.at  
Figure 3715: PRO95358  
Figure 3716: DNA330470, 096828.1, 222307.at  
Figure 3717: PRO85668  
Figure 3718: DNA344787, 016338.1, 222371.at  
Figure 3719: PRO95359  
Figure 3720A-B: DNA324364, NP\_037468.1, 222385.x.at  
Figure 3721: PRO1314  
Figure 3722: DNA335675, AJ251830, 222392.x.at  
Figure 3723: PRO90003  
Figure 3724: DNA227358, NP\_057479.1, 222404.x.at  
Figure 3725: PRO37821  
Figure 3726: DNA344788, AK074898, 222405.at  
Figure 3727: PRO95360  
Figure 3728A-B: DNA344789, NM\_014325, 222409.at  
Figure 3729: PRO49875  
Figure 3730: DNA327939, NP\_060654.1, 222442.s.at  
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Figure 3733: PRO37600  
Figure 3734A-B: DNA325652, NM\_016357, 222457.s.at  
Figure 3735: PRO82143  
Figure 3736A-B: DNA256489, NP\_079110.1, 222464.s.at  
Figure 3737: PRO51526  
Figure 3738: DNA331089, NP\_057143.1, 222500.at  
Figure 3739: PRO4984  
Figure 3740: DNA329370, NP\_060611.2, 222522.x.at  
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Figure 3742A-B: DNA344791, AL834191, 222603.at  
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Figure 3744: DNA330483, AK001472, 222608.s.at  
Figure 3745: PRO85679  
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Figure 3748: DNA344792, BC035985, 222622.at  
Figure 3749: PRO95362  
Figure 3750: DNA329331, NP\_005763.2, 222666.s.at  
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Figure 3753: PRO95363  
Figure 3754: DNA344794, NP\_079170.1, 222684.s.at  
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Figure 3756A-B: DNA344795, AF537091, 222685.at  
Figure 3757: PRO95365  
Figure 3758A-B: DNA344796, 998337.2, 222689.at  
Figure 3759: PRO95366  
Figure 3760: DNA339537, NM\_018394, 222697.s.at  
Figure 3761: PRO91303  
Figure 3762: DNA323797, NP\_078916.1, 222703.s.at  
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Figure 3764: DNA344797, BC044575, 222734.at  
Figure 3765: PRO95367  
Figure 3766: DNA333586, 295181.4, 222735.at  
Figure 3767: PRO84603  
Figure 3768A-B: DNA344798, NM\_014109, 222740.at  
Figure 3769: PRO95368  
Figure 3770: DNA335239, NM\_017688, 222746.s.at  
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Figure 3774: DNA344799, BC005401, 222763.s.at  
Figure 3775: PRO95369  
Figure 3776A-B: DNA335042, NM\_018092, 222774.s.at  
Figure 3777: PRO4401  
Figure 3778A-B: DNA344800, BC033901, 222787.s.at  
Figure 3779: PRO95370  
Figure 3780: DNA255044, DNA255044, 222833.at  
Figure 3781A-B: DNA329438, NP\_476516.1, 222837.s.at  
Figure 3782: PRO85008  
Figure 3783: DNA339367, NP\_037469.1, 222841.s.at  
Figure 3784: PRO91172  
Figure 3785: DNA344801, AL834387, 222843.at  
Figure 3786: PRO95371  
Figure 3787A-B: DNA333626, DNA333626, 222846.at  
Figure 3788: PRO88268  
Figure 3789: DNA335638, NP\_203130.1, 222847.s.at  
Figure 3790: PRO48216  
Figure 3791: DNA331389, NP\_071428.2, 222848.at  
Figure 3792: PRO81238  
Figure 3793A-B: DNA344802, NP\_064547.2, 222875.at  
Figure 3794: PRO95372  
Figure 3795: DNA344803, 321334.4, 222900.at  
Figure 3796: PRO95373  
Figure 3797: DNA344804, NP\_005012.1, 222938.x.at  
Figure 3798: PRO95374  
Figure 3799: DNA330501, AK022792, 222958.s.at  
Figure 3800: PRO85694  
Figure 3801: DNA330503, NP\_038466.2, 222991.s.at  
Figure 3802: PRO85696  
Figure 3803: DNA330504, NP\_057575.2, 222993.at  
Figure 3804: PRO84923  
Figure 3805: DNA324548, NP\_110409.2, 223020.at  
Figure 3806: PRO81202  
Figure 3807A-B: DNA344805, NP\_057308.1, 223027.at

- Figure 3808: PRO84924  
Figure 3809A-B: DNA344806, NM\_016224,  
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Figure 3811: DNA324707, NP\_037369.1, 223032\_x\_at  
Figure 3812: PRO81339  
Figure 3813A-B: DNA256347, NP\_065801.1,  
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Figure 3814: PRO51389  
Figure 3815A-B: DNA256347, NM\_020750,  
223056\_s\_at  
Figure 3816: PRO51389  
Figure 3817: DNA325295, NP\_113641.1, 223058\_at  
Figure 3818: PRO81841  
Figure 3819: DNA287216, NM\_021154, 223062\_s\_at  
Figure 3820: PRO69496  
Figure 3821: DNA304492, NP\_114405.1, 223065\_s\_at  
Figure 3822: PRO1864  
Figure 3823A-B: DNA328934, NP\_061936.2,  
223068\_at  
Figure 3824: PRO84649  
Figure 3825A-B: DNA328934, NM\_019063,  
223069\_s\_at  
Figure 3826: PRO84649  
Figure 3827: DNA344807, NP\_036609.1, 223072\_s\_at  
Figure 3828: PRO95375  
Figure 3829: DNA227294, NP\_060225.1, 223076\_s\_at  
Figure 3830: PRO37757  
Figure 3831A-B: DNA329316, AF158555,  
223079\_s\_at  
Figure 3832: PRO84904  
Figure 3833: DNA329349, NP\_054861.1, 223100\_s\_at  
Figure 3834: PRO84931  
Figure 3835A-C: DNA339662, NP\_110433.1,  
223125\_s\_at  
Figure 3836: PRO91404  
Figure 3837: DNA330445, NP\_112174.1, 223132\_s\_at  
Figure 3838: PRO85646  
Figure 3839: DNA325557, NP\_115675.1, 223151\_at  
Figure 3840: PRO82060  
Figure 3841: DNA329352, NP\_057154.2, 223156\_at  
Figure 3842: PRO84932  
Figure 3843A-B: DNA339969, BAA86461.1,  
223162\_s\_at  
Figure 3844: PRO91477  
Figure 3845: DNA324924, NP\_113631.1, 223164\_at  
Figure 3846: PRO81525  
Figure 3847A-B: DNA344808, NP\_067028.1,  
223168\_at  
Figure 3848: PRO1200  
Figure 3849A-B: DNA344809, AAH23525.1,  
223176\_at  
Figure 3850: PRO95376  
Figure 3851: DNA344810, NP\_113665.1, 223179\_at  
Figure 3852: PRO84933  
Figure 3853: DNA254276, NP\_054896.1, 223180\_s\_at  
Figure 3854: PRO49387  
Figure 3855: DNA344811, NP\_113675.2, 223182\_s\_at  
Figure 3856: PRO95377  
Figure 3857: DNA344812, AF201944, 223193\_x\_at  
Figure 3858: PRO95378  
Figure 3859: DNA323792, NP\_113647.1, 223195\_s\_at  
Figure 3860: PRO80542  
Figure 3861: DNA339535, NP\_060855.1, 223200\_s\_at  
Figure 3862: PRO91301  
Figure 3863A-B: DNA257461, NP\_113607.1,  
223217\_s\_at  
Figure 3864: PRO52040  
Figure 3865A-B: DNA257461, NM\_031419,  
223218\_s\_at  
Figure 3866: PRO52040  
Figure 3867: DNA327954, NP\_113646.1, 223220\_s\_at  
Figure 3868: PRO83879  
Figure 3869: DNA340182, NP\_068380.1, 223222\_at  
Figure 3870: PRO91677  
Figure 3871: DNA344813, NP\_114091.2, 223227\_at  
Figure 3872: PRO95379  
Figure 3873: DNA344814, NP\_060019.1, 223253\_at  
Figure 3874: PRO95380  
Figure 3875: DNA330517, NP\_115879.1, 223273\_at  
Figure 3876: PRO85707  
Figure 3877: DNA344815, NP\_116565.1, 223276\_at  
Figure 3878: PRO12050  
Figure 3879A-B: DNA330522, NP\_116071.2,  
223287\_s\_at  
Figure 3880: PRO85712  
Figure 3881: DNA326962, NP\_064711.1, 223290\_at  
Figure 3882: PRO83275  
Figure 3883: DNA330523, BC001220, 223294\_at  
Figure 3884: PRO85713  
Figure 3885: DNA257363, NP\_115691.1, 223296\_at  
Figure 3886: PRO51950  
Figure 3887: DNA329355, NP\_150596.1, 223299\_at  
Figure 3888: PRO50434  
Figure 3889: DNA329356, NP\_115671.1, 223304\_at  
Figure 3890: PRO84935  
Figure 3891: DNA330454, NP\_112589.1, 223307\_at  
Figure 3892: PRO85655  
Figure 3893: DNA344816, NM\_020806, 223319\_at  
Figure 3894: PRO50495  
Figure 3895: DNA329358, NP\_115649.1, 223334\_at  
Figure 3896: PRO84937  
Figure 3897A-B: DNA255756, L12052, 223358\_s\_at  
Figure 3898: PRO50812  
Figure 3899: DNA344817, NM\_145071, 223377\_x\_at  
Figure 3900: PRO86458  
Figure 3901A-B: DNA344818, NP\_055387.1,  
223380\_s\_at  
Figure 3902: PRO95381  
Figure 3903: DNA344819, NP\_663735.1, 223381\_at  
Figure 3904: PRO38881  
Figure 3905A-B: DNA344820, NP\_115644.1,

223382.s\_at  
Figure 3906: PRO84939  
Figure 3907A-B: DNA344821, NM\_032268,  
223383\_at  
Figure 3908: PRO84939  
Figure 3909: DNA340216, NP\_115686.2, 223398\_at  
Figure 3910: PRO91711  
Figure 3911: DNA339511, NP\_060635.1, 223400\_s.at  
Figure 3912: PRO91282  
Figure 3913: DNA324156, NP\_115588.1, 223403\_s.at  
Figure 3914: PRO80856  
Figure 3915: DNA344822, NP\_115514.2, 223412\_at  
Figure 3916: PRO95382  
Figure 3917: DNA329362, NP\_060286.1, 223413\_s.at  
Figure 3918: PRO84941  
Figure 3919: DNA329362, NM\_017816, 223414\_s.at  
Figure 3920: PRO84941  
Figure 3921: DNA255676, NP\_060754.1, 223434\_at  
Figure 3922: PRO50738  
Figure 3923: DNA330533, NP\_058647.1, 223451\_s.at  
Figure 3924: PRO772  
Figure 3925: DNA344823, BAA92078.1, 223457\_at  
Figure 3926: PRO95383  
Figure 3927: DNA273418, AAG01157.1, 223480\_s.at  
Figure 3928: DNA327958, NP\_115789.1, 223484\_at  
Figure 3929: PRO23554  
Figure 3930: DNA329456, NP\_057126.1, 223490\_s.at  
Figure 3931: PRO85023  
Figure 3932: DNA338084, NP\_006564.1, 223502\_s.at  
Figure 3933: PRO738  
Figure 3934: DNA344824, AF255647, 223503\_at  
Figure 3935: PRO95384  
Figure 3936: DNA333656, NP\_115646.2, 223533\_at  
Figure 3937: PRO88295  
Figure 3938: DNA330536, NP\_115666.1, 223542\_at  
Figure 3939: PRO85722  
Figure 3940A-B: DNA339971, BAA86587.1,  
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Figure 3942: DNA327028, NP\_005291.1, 223620\_at  
Figure 3943: PRO37083  
Figure 3944: DNA344825, BC002724, 223666\_at  
Figure 3945: PRO83126  
Figure 3946: DNA344826, NP\_006548.1, 223704\_s.at  
Figure 3947: PRO51385  
Figure 3948: DNA344827, AF176013, 223722\_at  
Figure 3949: PRO95385  
Figure 3950: DNA344828, NM\_146388, 223743\_s.at  
Figure 3951: PRO95386  
Figure 3952: DNA188735, NP\_001506.1, 223758\_s.at  
Figure 3953: PRO26224  
Figure 3954: DNA287253, NP\_444268.1, 223774\_at  
Figure 3955: PRO69527  
Figure 3956: DNA331132, NP\_115524.1, 223798\_at  
Figure 3957: PRO86273  
Figure 3958: DNA332645, NP\_570138.1, 223809\_at  
Figure 3959: PRO61997  
Figure 3960: DNA327200, NP\_114156.1, 223836\_at  
Figure 3961: PRO1065  
Figure 3962: DNA344829, NP\_683699.1, 223851\_s.at  
Figure 3963: PRO95387  
Figure 3964: DNA335398, AF132202, 223940\_x\_at  
Figure 3965A-B: DNA344830, NM\_004830,  
223947\_s.at  
Figure 3966: PRO95388  
Figure 3967: DNA335568, NM\_024022, 223948\_s.at  
Figure 3968: PRO89910  
Figure 3969: DNA327213, NM\_032405, 223949\_at  
Figure 3970: PRO83482  
Figure 3971: DNA344831, NM\_013324, 223961\_s.at  
Figure 3972: PRO37588  
Figure 3973: DNA324248, NM\_004509, 223980\_s.at  
Figure 3974: PRO80932  
Figure 3975: DNA344832, AF130059, 223991\_s.at  
Figure 3976: PRO95389  
Figure 3977: DNA344833, NP\_002594.1, 224046\_s.at  
Figure 3978: PRO95390  
Figure 3979: DNA344834, NM\_172234, 224156\_x\_at  
Figure 3980: PRO95391  
Figure 3981A-C: DNA227619, NP\_054831.1,  
224218\_s.at  
Figure 3982: PRO38082  
Figure 3983: DNA324707, NM\_013237, 224232\_s.at  
Figure 3984: PRO81339  
Figure 3985: DNA329370, NM\_018141, 224247\_s.at  
Figure 3986: PRO84949  
Figure 3987: DNA344835, NP\_115942.1, 224285\_at  
Figure 3988: PRO78450  
Figure 3989: DNA330558, NP\_057588.1, 224330\_s.at  
Figure 3990: PRO84950  
Figure 3991: DNA344836, NP\_115868.1, 224331\_s.at  
Figure 3992: PRO84951  
Figure 3993: DNA344837, BC015060, 224345\_x\_at  
Figure 3994: PRO86616  
Figure 3995: DNA344838, NM\_018725, 224361\_s.at  
Figure 3996: PRO19612  
Figure 3997: DNA335328, NP\_116010.1, 224367\_at  
Figure 3998: PRO89703  
Figure 3999: DNA330334, NP\_114402.1, 224368\_s.at  
Figure 4000: PRO85557  
Figure 4001: DNA328323, NP\_114148.2, 224428\_s.at  
Figure 4002: PRO69531  
Figure 4003: DNA344839, NP\_113668.2, 224450\_s.at  
Figure 4004: PRO95392  
Figure 4005: DNA328885, NM\_018638, 224453\_s.at  
Figure 4006: PRO50294  
Figure 4007: DNA344840, NP\_116186.1, 224461\_s.at  
Figure 4008: PRO95393  
Figure 4009: DNA329373, NP\_115722.1, 224467\_s.at  
Figure 4010: PRO84952  
Figure 4011: DNA323732, NP\_057260.2, 224472\_x\_at  
Figure 4012: PRO80490

- Figure 4013: DNA344841, BC006236, 224480.s.at  
Figure 4014: PRO95394  
Figure 4015A-C: DNA344842, AJ314646, 224482.s.at  
Figure 4016: DNA344843, BC006384, 224507.s.at  
Figure 4017: PRO95396  
Figure 4018: DNA344844, 242250.1, 224508.at  
Figure 4019: PRO95397  
Figure 4020: DNA327977, NP\_115886.1, 224518.s.at  
Figure 4021: PRO83898  
Figure 4022: DNA329374, NP\_115735.1, 224523.s.at  
Figure 4023: PRO84953  
Figure 4024: DNA344845, NM\_148902, 224553.s.at  
Figure 4025: PRO95398  
Figure 4026: DNA344846, 1453417.19, 224559.at  
Figure 4027: PRO95399  
Figure 4028A-E: DNA344847, AF001893, 224566.at  
Figure 4029: PRO95400  
Figure 4030: DNA334965, D87666, 224567.x.at  
Figure 4031: DNA330569, BC020516, 224572.s.at  
Figure 4032: DNA344848, NP\_066972.1, 224583.at  
Figure 4033: PRO82633  
Figure 4034A-B: DNA334919, NP\_536856.2, 224596.at  
Figure 4035: PRO89354  
Figure 4036: DNA344849, 1383705.7, 224601.at  
Figure 4037: PRO95401  
Figure 4038: DNA331396, 1357555.1, 224603.at  
Figure 4039: PRO86461  
Figure 4040: DNA255362, DNA255362, 224604.at  
Figure 4041: DNA344850, BC017399, 224605.at  
Figure 4042: PRO95402  
Figure 4043: DNA344851, AF070636, 224609.at  
Figure 4044: PRO95403  
Figure 4045: DNA344852, 348196.115, 224610.at  
Figure 4046: PRO95404  
Figure 4047: DNA329376, BAA91036.1, 224632.at  
Figure 4048: PRO84954  
Figure 4049A-B: DNA344853, 361207.5, 224634.at  
Figure 4050: PRO95405  
Figure 4051: DNA344854, AK093442, 224654.at  
Figure 4052: PRO95406  
Figure 4053A-B: DNA344855, BAB21782.1, 224674.at  
Figure 4054: PRO49364  
Figure 4055A-B: DNA344856, AL161973, 224685.at  
Figure 4056A-B: DNA330574, BAA86542.2, 224698.at  
Figure 4057: PRO85755  
Figure 4058: DNA329378, BC022990, 224714.at  
Figure 4059: PRO84956  
Figure 4060: DNA330577, NP\_443076.1, 224715.at  
Figure 4061: PRO85758  
Figure 4062: DNA330579, NP\_612434.1, 224719.s.at  
Figure 4063: PRO85760  
Figure 4064: DNA344857, NP\_653202.1, 224733.at  
Figure 4065: PRO95408  
Figure 4066: DNA257352, DNA257352, 224739.at  
Figure 4067: PRO51940  
Figure 4068: DNA344858, 887619.58, 224741.x.at  
Figure 4069: PRO95409  
Figure 4070: DNA330581, NP\_542399.1, 224753.at  
Figure 4071: PRO82014  
Figure 4072A-B: DNA344859, NP\_065875.1, 224764.at  
Figure 4073: PRO95410  
Figure 4074: DNA336077, BC035511, 224783.at  
Figure 4075: PRO90299  
Figure 4076A-B: DNA333692, AB033075, 224790.at  
Figure 4077: DNA228087, DNA228087, 224793.s.at  
Figure 4078: PRO38550  
Figure 4079A-B: DNA287330, BAA86479.1, 224799.at  
Figure 4080: PRO69594  
Figure 4081A-B: DNA330584, NP\_065881.1, 224800.at  
Figure 4082: PRO85764  
Figure 4083A-B: DNA287330, AB032991, 224801.at  
Figure 4084: DNA331397, AK001723, 224802.at  
Figure 4085: PRO23259  
Figure 4086: DNA344860, NP\_699164.1, 224819.at  
Figure 4087: PRO95411  
Figure 4088A-B: DNA330559, BAB21791.1, 224832.at  
Figure 4089: PRO85741  
Figure 4090A-B: DNA330809, 336997.1, 224837.at  
Figure 4091: PRO85973  
Figure 4092A-B: DNA330522, NM\_032682, 224838.at  
Figure 4093: PRO85712  
Figure 4094A-B: DNA344861, NP\_597700.1, 224839.s.at  
Figure 4095: PRO95412  
Figure 4096A-B: DNA324748, NP\_004108.1, 224840.at  
Figure 4097: PRO36841  
Figure 4098A-B: DNA344862, AF141346, 224841.x.at  
Figure 4099: DNA344863, BC027989, 224847.at  
Figure 4100: PRO95414  
Figure 4101A-C: DNA329379, 010205.2, 224848.at  
Figure 4102: PRO84957  
Figure 4103: DNA344864, NP\_116199.1, 224850.at  
Figure 4104: PRO95415  
Figure 4105A-B: DNA324748, NM\_004117, 224856.at  
Figure 4106: PRO36841  
Figure 4107: DNA329381, D28589, 224870.at  
Figure 4108A-B: DNA344865, NP\_065871.1, 224909.s.at  
Figure 4109: PRO95416  
Figure 4110: DNA344866, AAH10736.1, 224913.s.at  
Figure 4111: PRO95417

- Figure 4112: DNA330591, NP\_115865.1, 224919\_at  
Figure 4113: PRO85771  
Figure 4114A-B: DNA344867, BC009948, 224925\_at  
Figure 4115: PRO95418  
Figure 4116A-B: DNA228196, BAA92674.1, 224937\_at  
Figure 4117: PRO38661  
Figure 4118: DNA336269, 346724.14, 224944\_at  
Figure 4119: PRO90430  
Figure 4120: DNA344868, 7769724.1, 224989\_at  
Figure 4121: PRO95419  
Figure 4122: DNA329384, NP\_777581.1, 224990\_at  
Figure 4123: PRO84960  
Figure 4124: DNA344869, BC034247, 225036\_at  
Figure 4125: PRO95420  
Figure 4126: DNA344870, NP\_061189.1, 225081\_s\_at  
Figure 4127: PRO95421  
Figure 4128: DNA330598, 1384569.2, 225086\_at  
Figure 4129: PRO85776  
Figure 4130A-E: DNA329391, 233747.10, 225097\_at  
Figure 4131: PRO84967  
Figure 4132A-B: DNA327993, 898436.7, 225133\_at  
Figure 4133: PRO81138  
Figure 4134: DNA344871, BC037573, 225148\_at  
Figure 4135: PRO95422  
Figure 4136: DNA344872, NP\_079272.4, 225158\_at  
Figure 4137: PRO84969  
Figure 4138: DNA344873, NM\_024996, 225161\_at  
Figure 4139: PRO84969  
Figure 4140: DNA330604, NP\_277050.1, 225171\_at  
Figure 4141: PRO85782  
Figure 4142: DNA330604, NM\_033515, 225173\_at  
Figure 4143: PRO85782  
Figure 4144: DNA344874, BC040556, 225175\_s\_at  
Figure 4145: PRO95423  
Figure 4146: DNA344875, AAH27990.1, 225178\_at  
Figure 4147: PRO83914  
Figure 4148A-B: DNA344876, 335186.18, 225195\_at  
Figure 4149: PRO95424  
Figure 4150: DNA336053, NP\_110438.1, 225196\_s\_at  
Figure 4151: PRO90282  
Figure 4152: DNA344877, 233597.34, 225220\_at  
Figure 4153: PRO95425  
Figure 4154: DNA344878, NP\_542763.1, 225252\_at  
Figure 4155: PRO95426  
Figure 4156A-B: DNA330605, 233102.7, 225265\_at  
Figure 4157: PRO85783  
Figure 4158A-B: DNA258863, DNA258863, 225266\_at  
Figure 4159A-B: DNA344879, 7771332.17, 225285\_at  
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Figure 4534: PRO95530

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Figure 4593: PRO95547  
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Figure 4607: PRO23647  
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Figure 4615: PRO12014  
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Figure 4619: PRO92247  
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Figure 4649: PRO85927  
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Figure 4655: PRO85928  
Figure 4656A-B: DNA328454, NP\_057525.1, 228496\_s\_at  
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Figure 4658: DNA345024, 412954.22, 228532\_at  
Figure 4659: PRO95560  
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Figure 4665: PRO4644  
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Figure 4683: DNA330777, DNA330777, 228869\_at  
Figure 4684: PRO85941  
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Figure 4714: PRO87337  
Figure 4715A-B: DNA345036, 468481.1, 229116\_at  
Figure 4716: PRO95572  
Figure 4717A-D: DNA345037, 903479.18, 229287\_at  
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Figure 4733: PRO84001  
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Figure 4737: PRO90970  
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Figure 4743: PRO95575  
Figure 4744A-B: DNA345041, AL834393, 229594\_at  
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Figure 4750: PRO95579  
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- Figure 4752: PRO88384  
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Figure 4756: DNA334491, 428695.5, 229725\_at  
Figure 4757: PRO88993  
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Figure 4763: PRO85971  
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Figure 4765: PRO95583  
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Figure 4767: PRO81858  
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Figure 4770: DNA345050, 221062.1, 229954\_at  
Figure 4771: PRO95584  
Figure 4772A-B: DNA345051, NP\_722579.1, 229971\_at  
Figure 4773: PRO6017  
Figure 4774: DNA345052, NP\_689413.1, 229980\_s\_at  
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Figure 4782: DNA332487, DNA332487, 230110\_at  
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Figure 4784: DNA345054, 064937.11, 230141\_at  
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Figure 4786: DNA345055, NP\_065391.1, 230170\_at  
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Figure 4789: PRO95587  
Figure 4790A-B: DNA345057, AL713763, 230180\_at  
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Figure 4792: DNA345058, AL832695, 230192\_at  
Figure 4793: DNA345059, 229293.16, 230206\_at  
Figure 4794: PRO95590  
Figure 4795: DNA345060, 7692383.1, 230226\_s\_at  
Figure 4796: PRO95591  
Figure 4797: DNA345061, AK058039, 230292\_at  
Figure 4798: PRO95592  
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Figure 4804: PRO85986  
Figure 4805A-B: DNA345063, 234102.72, 230425\_at  
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Figure 4807: DNA345064, NP\_653312.1, 230434\_at  
Figure 4808: PRO95595  
Figure 4809: DNA330712, 1452648.12, 230466\_s\_at  
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Figure 4811A-B: DNA330824, 333480.5, 230489\_at  
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Figure 4816: PRO87594  
Figure 4817: DNA345065, 234921.2, 230570\_at  
Figure 4818: PRO95596  
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Figure 4826: PRO91742  
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Figure 4828: PRO95597  
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Figure 4832: PRO95598  
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Figure 4834: PRO87470  
Figure 4835: DNA338109, 211204.3, 230866\_at  
Figure 4836: PRO90980  
Figure 4837: DNA336019, DNA336019, 230970\_at  
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Figure 4840: DNA329405, AL117452, 231094\_s\_at  
Figure 4841: DNA345069, 895820.1, 231106\_at  
Figure 4842: PRO95600  
Figure 4843: DNA329473, 370473.13, 231124\_x\_at  
Figure 4844: PRO85038  
Figure 4845A-B: DNA226303, DNA226303, 231259\_s\_at  
Figure 4846: PRO36766  
Figure 4847A-B: DNA339703, NP\_115970.2, 231396\_s\_at  
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Figure 4849: DNA338354, DNA338354, 231576\_at  
Figure 4850: PRO91025  
Figure 4851: DNA150808, M55542, 231577\_s\_at  
Figure 4852: PRO12478  
Figure 4853: DNA345070, NP\_006630.1, 231747\_at  
Figure 4854: PRO34958  
Figure 4855: DNA330839, NP\_060908.1, 231769\_at  
Figure 4856: PRO86002  
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Figure 4858: PRO50745

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Figure 4866: PRO85040  
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Figure 4869: DNA345072, 978672.3, 232000\_at  
Figure 4870: PRO95602  
Figure 4871: DNA345073, NP\_056475.1, 232024\_at  
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Figure 4876: PRO86015  
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Figure 4880: PRO95604  
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Figure 4882: PRO95605  
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Figure 4886: PRO86025  
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Figure 4892: DNA329286, NP\_005691.2, 232510\_s\_at  
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Figure 4894: DNA330868, 337037.1, 232584\_at  
Figure 4895: PRO86031  
Figure 4896: DNA340361, DNA340361, 232615\_at  
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Figure 4903: DNA330870, 227719.1, 232883\_at  
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Figure 4908: PRO95607  
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Figure 4912: PRO91663  
Figure 4913: DNA324156, NM\_032212, 233341\_s\_at  
Figure 4914: PRO80856  
Figure 4915: DNA331423, AF176071, 233467\_s\_at  
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Figure 4917: PRO49998  
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Figure 4919: PRO89830  
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Figure 4921: PRO95608  
Figure 4922: DNA329481, NM\_016150, 233857\_s\_at  
Figure 4923: PRO60949  
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Figure 4925: PRO90981  
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Figure 4929: PRO86682  
Figure 4930: DNA333607, 211626.1, 234151\_at  
Figure 4931: PRO88251  
Figure 4932: DNA345080, 401293.1, 234260\_at  
Figure 4933: PRO95609  
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Figure 4935: PRO95610  
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Figure 4943: PRO95612  
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Figure 4945: PRO20110  
Figure 4946: DNA345085, AAA61109.1, 234440\_at  
Figure 4947: PRO95613  
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Figure 4951: PRO95614  
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Figure 4953: PRO95615  
Figure 4954: DNA345088, CAA29554.1, 234849\_at  
Figure 4955: PRO95616  
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Figure 4957: PRO95617  
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Figure 4959: PRO86044  
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Figure 4961: PRO95618

- Figure 4962: DNA258761, DNA258761, 235019\_at  
Figure 4963A-B: DNA345091, 135369.13, 235020\_at  
Figure 4964: PRO95619  
Figure 4965: DNA339413, DNA339413, 235046\_at  
Figure 4966A-B: DNA345092, 292261.1, 235048\_at  
Figure 4967: PRO95620  
Figure 4968A-B: DNA340485, BAC56923.1, 235085\_at  
Figure 4969: PRO92206  
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Figure 4975: PRO88377  
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Figure 4978: DNA330896, 250896.1, 235213\_at  
Figure 4979: PRO86057  
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Figure 4981: PRO95623  
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Figure 4983: PRO80802  
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Figure 4988: PRO86059  
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Figure 4995A-B: DNA345099, AF133211, 235421\_at  
Figure 4996: PRO95626  
Figure 4997A-B: DNA345100, NP\_689737.1, 235425\_at  
Figure 4998: PRO95627  
Figure 4999A-B: DNA345101, 979268.1, 235440\_at  
Figure 5000: PRO95628  
Figure 5001: DNA257872, DNA257872, 235457\_at  
Figure 5002: DNA330906, NP\_116171.2, 235458\_at  
Figure 5003: PRO86067  
Figure 5004A-B: DNA345102, AAH30800.1, 235463\_s\_at  
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Figure 5006: DNA345103, NP\_689629.1, 235509\_at  
Figure 5007: PRO95630  
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Figure 5009: PRO86073  
Figure 5010A-B: DNA336026, AB095926, 235643\_at  
Figure 5011: DNA345104, 1448915.1, 235680\_at  
Figure 5012: PRO95631  
Figure 5013: DNA336165, AF368463, 235706\_at  
Figure 5014: PRO84371  
Figure 5015: DNA345105, NP\_689674.1, 235745\_at  
Figure 5016: PRO95632  
Figure 5017A-B: DNA335175, DNA335175, 235971\_at  
Figure 5018: PRO89566  
Figure 5019A-B: DNA345106, 244378.1, 236125\_at  
Figure 5020: PRO49375  
Figure 5021: DNA336348, 1512910.2, 236203\_at  
Figure 5022: PRO90492  
Figure 5023: DNA331211, 392245.1, 236226\_at  
Figure 5024: PRO86341  
Figure 5025: DNA335691, DNA335691, 236280\_at  
Figure 5026: PRO12646  
Figure 5027: DNA345107, AF488410, 236313\_at  
Figure 5028A-B: DNA345108, AF318353, 236322\_at  
Figure 5029: PRO95634  
Figure 5030: DNA329312, AF414120, 236341\_at  
Figure 5031: PRO84901  
Figure 5032: DNA333653, 325998.1, 236435\_at  
Figure 5033: PRO88292  
Figure 5034: DNA345109, 7763130.1, 236471\_at  
Figure 5035: PRO95635  
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Figure 5037: PRO84071  
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Figure 5040: DNA330934, DNA330934, 236595\_at  
Figure 5041: PRO86095  
Figure 5042: DNA330935, 229915.1, 236610\_at  
Figure 5043: PRO86096  
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Figure 5045: PRO95637  
Figure 5046: DNA329491, DNA329491, 236787\_at  
Figure 5047: DNA330939, 214517.1, 236796\_at  
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Figure 5049: DNA345112, AK074237, 236984\_at  
Figure 5050: PRO95638  
Figure 5051: DNA330943, 1042935.2, 237009\_at  
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Figure 5054: PRO95639  
Figure 5055A-B: DNA226536, NM\_003234, 237215\_s\_at  
Figure 5056: PRO36999  
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Figure 5058: PRO78081  
Figure 5059: DNA328178, 985267.1, 237839\_at  
Figure 5060: PRO84081  
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Figure 5062: PRO86111  
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Figure 5064: PRO60111  
Figure 5065: DNA345116, BC033490, 238018\_at  
Figure 5066: PRO95640  
Figure 5067A-B: DNA330952, 333610.10,

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Figure 5070: PRO95641  
Figure 5071: DNA345118, 337083.5, 238075.at  
Figure 5072: PRO95642  
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Figure 5075: DNA345119, 331249.6, 238520.at  
Figure 5076: PRO95643  
Figure 5077: DNA329495, 1447201.1, 238581.at  
Figure 5078: PRO85056  
Figure 5079: DNA329497, 232064.1, 238619.at  
Figure 5080: PRO85058  
Figure 5081A-B: DNA345120, 1400266.11, 238649.at  
Figure 5082: PRO95644  
Figure 5083: DNA334895, 172305.1, 238787.at  
Figure 5084: PRO89333  
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Figure 5086: PRO84091  
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Figure 5088: PRO95645  
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Figure 5090: PRO85061  
Figure 5091A-C: DNA345122, NM\_018136,  
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Figure 5092: PRO95646  
Figure 5093A-B: DNA345123, 086440.4, 239151.at  
Figure 5094: PRO95647  
Figure 5095: DNA335753, 408088.2, 239179.at  
Figure 5096: PRO90062  
Figure 5097: DNA345124, 7685093.8, 239237.at  
Figure 5098: PRO95648  
Figure 5099: DNA345125, 401336.15, 239288.at  
Figure 5100: PRO95649  
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Figure 5102: PRO88371  
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Figure 5104: PRO95650  
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Figure 5106: PRO85063  
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Figure 5110: PRO95651  
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Figure 5112: PRO88274  
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Figure 5114: PRO85538  
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Figure 5116: PRO91765  
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Figure 5120: PRO95652  
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Figure 5124: PRO95654  
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Figure 5126: PRO95655  
Figure 5127: DNA345133, BC016950, 241682.at  
Figure 5128: PRO95656  
Figure 5129: DNA345134, 212515.1, 241819.at  
Figure 5130: PRO24261  
Figure 5131: DNA331011, 979953.1, 241859.at  
Figure 5132: PRO86169  
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Figure 5142: PRO95659  
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Figure 5144: PRO95660  
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Figure 5155: PRO89696  
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Figure 5159: PRO95664  
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Figure 5195: PRO95672  
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Figure 5499: PRO3637  
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Figure 5542: PRO2620  
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Figure 5554: PRO12570  
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Figure 5576: PRO20114  
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Figure 5582: PRO12839  
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 Figure 5592: PRO4538  
 Figure 5593: DNA287620, NM\_004131,  
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 Figure 5596: PRO38025  
 Figure 5597: DNA331392, NM\_004195,  
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 Figure 5598: PRO364  
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 Figure 5606: PRO20124  
 Figure 5607: DNA287240, NM\_004335,  
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 Figure 5608: PRO29371  
 Figure 5609: DNA329008, NP\_004337.2,  
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 Figure 5623: DNA226737, NM\_004585,  
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 Figure 5655: DNA189700, NM\_005252,  
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Figure 5903: PRO84623

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Figure 6464: PRO53782

What is claimed:

1. Isolated nucleic acid comprising at least 80% nucleic acid sequence identity to a nucleotide sequence encoding the polypeptide as shown in any one of the SEQ ID NOs 1-6464.

5

2. Isolated nucleic acid comprising at least 80% nucleic acid sequence identity to a nucleotide sequence comprising the full-length coding sequence of the nucleotide sequence as shown in any one of the SEQ ID NOs 1-6464.

10

3. A vector comprising the nucleic acid of Claim 1.

4. The vector of Claim 3 operably linked to control sequences recognized by a host cell transformed with the vector.

15

5. A host cell comprising the vector of Claim 3.

6. The host cell of Claim 5, wherein said cell is a CHO cell, an *E.coli* cell or a yeast cell.

20

7. A process for producing a PRO polypeptide comprising culturing the host cell of Claim 6 under conditions suitable for expression of said PRO polypeptide and recovering said PRO polypeptide from the cell culture.

8. An isolated polypeptide comprising at least 80% amino acid sequence identity to an amino acid sequence of the polypeptide as shown in any one of the SEQ ID NOs 1-6464.

25

9. A chimeric molecule comprising a polypeptide according to Claim 8 fused to a heterologous amino acid sequence.

30

10. The chimeric molecule of Claim 9, wherein said heterologous amino acid sequence is an epitope tag sequence or an Fc region of an immunoglobulin.

11. An antibody which specifically binds to a polypeptide according to Claim 8.

35

12. The antibody of Claim 11, wherein said antibody is a monoclonal antibody, a humanized antibody or a single-chain antibody.

13. A composition of matter comprising (a) a polypeptide of Claim 8, (b) an agonist of said polypeptide, (c) an antagonist of said polypeptide, or (d) an antibody that binds to said polypeptide, in combination with a carrier.

40

14. The composition of matter of Claim 13, wherein said carrier is a pharmaceutically acceptable carrier.

15. The composition of matter of Claim 14 comprising a therapeutically effective amount of  
5 (a), (b), (c) or (d).

16. An article of manufacture, comprising:

a container;  
a label on said container; and

10 a composition of matter comprising (a) a polypeptide of Claim 8, (b) an agonist of said polypeptide, (c) an antagonist of said polypeptide, or (d) an antibody that binds to said polypeptide, contained within said container; wherein label on said container indicates that said composition of matter can be used for treating an immune related disease.

15 17. A method of treating an immune related disorder in a mammal in need thereof comprising administering to said mammal a therapeutically effective amount of (a) a polypeptide of Claim 8, (b) an agonist of said polypeptide, (c) an antagonist of said polypeptide, or (d) an antibody that binds to said polypeptide.

20 18. The method of Claim 17, wherein the immune related disorder is systemic lupus erythematosis, rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis, a spondyloarthropathy, systemic sclerosis, an idiopathic inflammatory myopathy, Sjögren's syndrome, systemic vasculitis, sarcoidosis, autoimmune hemolytic anemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal disease, a demyelinating disease of the central or peripheral nervous system, 25 idiopathic demyelinating polyneuropathy, Guillain-Barré syndrome, a chronic inflammatory demyelinating polyneuropathy, a hepatobiliary disease, infectious or autoimmune chronic active hepatitis, primary biliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis, inflammatory bowel disease, gluten-sensitive enteropathy, Whipple's disease, an autoimmune or immune-mediated skin disease, a bullous skin disease, erythema multiforme, contact dermatitis, psoriasis, an allergic disease, asthma, allergic rhinitis, atopic 30 dermatitis, food hypersensitivity, urticaria, an immunologic disease of the lung, eosinophilic pneumonias, idiopathic pulmonary fibrosis, hypersensitivity pneumonitis, a transplantation associated disease, graft rejection or graft-versus-host-disease.

19. A method for determining the presence of a PRO polypeptide of the invention as described  
35 in any one of SEQ ID NOs 1-6464, in a sample suspected of containing said polypeptide, said method comprising exposing said sample to an anti-PRO antibody, where the and determining binding of said antibody to a component of said sample.

20. A method of diagnosing an immune related disease in a mammal, said method comprising  
40 detecting the level of expression of a gene encoding a PRO polypeptide of the invention as described in any

one of SEQ ID NOS 1-6464, (a) in a test sample of tissue cells obtained from the mammal, and (b) in a control sample of known normal tissue cells of the same cell type, wherein a higher or lower level of expression of said gene in the test sample as compared to the control sample is indicative of the presence of an immune related disease in the mammal from which the test tissue cells were obtained.

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21. A method of diagnosing an immune related disease in a mammal, said method comprising (a) contacting a PRO polypeptide of the invention as described in any one of SEQ ID NOS 1-6464, anti-PRO antibody with a test sample of tissue cells obtained from said mammal and (b) detecting the formation of a complex between the antibody and the polypeptide in the test sample, wherein formation of said complex is indicative of the presence of an immune related disease in the mammal from which the test tissue cells were obtained.

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22. A method of identifying a compound that inhibits the activity of a PRO polypeptide of the invention as described in any one of SEQ ID NOS 1-6464, said method comprising contacting cells which normally respond to said polypeptide with (a) said polypeptide and (b) a candidate compound, and determining the lack responsiveness by said cell to (a).

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23. A method of identifying a compound that inhibits the expression of a gene encoding a PRO polypeptide of the invention as described in any one of SEQ ID NOS 1-6464, said method comprising contacting cells which normally express said polypeptide with a candidate compound, and determining the lack of expression said gene.

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24. The method of Claim 23, wherein said candidate compound is an antisense nucleic acid.

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25. A method of identifying a compound that mimics the activity of a PRO polypeptide of the invention as described in any one of SEQ ID NOS 1-6464, said method comprising contacting cells which normally respond to said polypeptide with a candidate compound, and determining the responsiveness by said cell to said candidate compound.

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26. A method of stimulating the immune response in a mammal, said method comprising administering to said mammal an effective amount of a PRO polypeptide of the invention as described in any one of SEQ ID NOS 1-6464, antagonist, wherein said immune response is stimulated.

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27. A method of diagnosing an inflammatory immune response in a mammal, said method comprising detecting the level of expression of a gene encoding a PRO polypeptide of the invention as described in any one of SEQ ID NOS 1-6464, (a) in a test sample of tissue cells obtained from the mammal, and (b) in a control sample of known normal tissue cells of the same cell type, wherein a higher or lower level of expression of said gene in the test sample as compared to the control sample is indicative of the presence of an inflammatory immune response in the mammal from which the test tissue cells were obtained.

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